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Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                          No.
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                               and is derived by analysis of the total score distribution
                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                    86.5
88
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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(without alignments)
548.648 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283366 seqs, 96191526 residues
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Copyright (c) 1993 - 2004 Compugen Ltd.
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pir2:
pir3::*
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HSTR1R
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S61926
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S51364
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AE1317
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F90725
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                                                                       hypothetical prote
probable NLP/P60 f
probable zuotin (i
probable DNA topoi
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hypothetical prote
mst101-1 protein -
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                                                    histone H1 - trout
histone H1 - rainb
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                                                                                                                     asparaginyl-trna
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                                                                                                                                  -acylglycerol-3-p
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78 36.6 217 2 S29309 hypochetical protein 836.6 231 2 S59589 histone H1 - Chlam 78 36.6 287 2 S45662 histone H1 - tomat 78 36.6 287 2 S45662 histone H1 - tomat 78 36.6 309 2 G83013 polyhydroxyalkanoa 77.5 36.4 37.6 2 A60592 tolk protein (impo 77 36.2 220 2 A28456 histone H1.50 - ch 77 36.2 220 2 A28456 histone H1.50 - ch 77 36.2 220 2 B70868 histone H1.50 - ch 77 36.2 523 2 B38145 invariant surface 77 36.2 523 2 B70868 probable transfera 78 35.7 241 2 J00748 histone H1.7 - V0 35.7 249 2 J00748 Tolk colicin impor 75 35.2 212 2 A28470 histone H1- mouse 75 35.2 212 2 A28470 histone H1 - mouse 75 35.2 212 2 A28470 histone H1 - mouse	45	44	43	42	41	40	39	8	37	36	35	34	33	32	31
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\$29309 his separate with the s	212	924	220	388	241	229	580	523	226	220	376	309	287	231	217
nd 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	N	N	N	N	N	N	N	N	<b>μ</b>	N	N	N	N	N	N
hypo hist hist hist toll, hist investor hist hist hist hist hist hist hist hist	A28470	T06636	JC5954	AC0138	JN0748	I51227	B70868	B38145	S51660	A28456	AG0592	G83013	S45662	859589	S29309

#### ALIGNMENTS

R;Knowles, J.A.; Childs, G.J.
Nucleic Acids Res. 14, 8121-8133, 1986
A;Title: Comparison of the late H1 histone genes of the sea urchins Lytechinus pictus
A;Reference number: A25550; MUID:87040778; PMID:3022245
A;Accession: A25550

A; Molecule type: DNA A; Residues: 1-210 < KNO> histone H1 - sea urchin (Lytechinus pictus)
C;Species: Lytechinus pictus (painted urchin)
C;Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 23-Jul-1999
C;Accession: A25550

A25550

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DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and ger A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90725
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-394 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34197.1; PID:g13360233; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          membrane spanning protein TolA [imported] - Escherichia coli (strain 0157:H7, substrain 0;Species: Escherichia coli (c;Species: Bscherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: F90725
                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.@
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
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                                                                                                                                                                                C;Genetics:
A;Gene: ECs0774
                                                                             Query Match
Best Local S
Matches 32
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Best Local Similarity 65.1%;
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                                                                                                     Local Similarity
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1 AKKYAKKAKAEK-AKKAYKAAEAKKAAKYEKAAAEKAAAKEAA 42
                                                                                Conservative
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                                                                                                     46.0%;
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                                                                                                     Score 98; DB 2;
Pred. No. 0.028;
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                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Indels
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                                                                                                                           Length 394;
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220

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A;Cross-references: GB:M28232; NID:g148018; PIDN:AAA24683.1; PID:g148019
A;Experimental source: strain JM105
A;Experimental source: strain JM105
A;Note: the authors translated the initiation codon GTG for residue 1 as Val
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B64810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Escherichia coli
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Mar-2002
C;Accession: JV0057; B64810
R;Levengood, S.K.; Webster, R.E.
J. Bacteriol. 171, 6600-6609, 1989
A;Title: Nucleotide sequences of the tolA and tolB genes and localization of their produ A;Reference number: JV0057; MUID:90078104; PMID:2687247
A;Accession: JV0057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   멍
                                                                                                                                                                                                  A; Map position: 17 min
A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AAC73833.1; PID:g1786960; A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ś
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-421 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE005174; NID:g12513672; PIDN:AAG55075.1; GSPDB:GN00145; UWGP:Z09
A;Experimental source: strain C157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-394 <STO>
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A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, S.; Potamousis,
Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: G85576
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose,
                                                                                                               Keywords: nucleotide binding; P-loop; transmembrane protein;14-34/Domain: transmembrane #status predicted <MSS>;78-301/Domain: helical #status predicted <HSR>
                       Query Match
Best Local Similarity
                                                                                                     355-362/Region:
                                                                                                                                                                                                                                                                               Genetics
                                                                                                                                                                                                                                                                                                    Comment: tolA and tolB proteins are necessary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli (strain K-12)
     Conservative
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                                                                                             nucleotide-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                            acid sequence not shown; translation not shown
                       46.0%;
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                       Score 98;
Pred. No.
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Pred. No. 0.028;
     Mismatches
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                       0.029;
                                             DB 2; Length 421;
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K.; Apodaca
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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; W. A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
Science 294, 849-852, 2001
Science 294, 849-852, 2001
Science 294, 849-852, 2001
Schutors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1117
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C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AE1317
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
R;Glaser, P.; Frangeul, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AL592022; PIDN:CAC97285.1; PID:g16414556; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin2055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AE1689
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:NC_003210; PIDN:CAD00019.1; PID:g16411394; GSPDB:GN00177 A;Experimental source: strain EGD-e C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-243 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: AE1689
A;Status: preliminary
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A; Residues: 1-239 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: lmo1941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein lmo1941 [imported] - Listeria monocytogenes (strain EGD-e)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein homolog lin2055 [imported] - Listeria innocua (strain Clip11262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
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166 DKAAKE 171
                                                                                                        106 AKKAAEEKAAAEKAAEEKKAAEEKAAADKKSQEDEAAKAAAAKKEQEAAEEKAAAEKAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 KAAAEKAEADKKKQEEDAVKAANAKKEQEAAEEKAAADKAAAEKAAAE 171
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                                                     39 KEAAYE 44
                                                                                                                                                           N
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27; Conser
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                                                                                                                                                                                                                                        Score 90;
Pred. No.
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                                                                                                                                                                                                                                                                 DB 2; Length 243;
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Wehland,
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probable hup8 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: G70673
R;Accession: G70673
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
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R;Lai, Z.C.; Childs, G.
Mol. Cell. Biol. 8, 1842-1844, 1988
Mol. Cell. Biol. 8, 1842-1844, 1988
A;Title: Characterization of the structure and transcriptional patterns of the gene enco
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A; Residues: 1-211 <LAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   histone H1-beta, embryonic - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 23-Feb-1997
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A;Residues: 1-163,'E',164-236,'Q',237-254,257-320,'E',321-1390 <NEW>
A;Cross-references: EMBL:X73481; NID:g313201; PID:g313202
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A;Cross-references: EMBL:X73481
R;Neesen, J.; Heillein, U.A.O.; Buenemann, submitted to the EMBL Data Library, June 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eur. J. Blochem. 225, 1089-1095, 1994
A,Title: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif represe lpha-helical rods within the extremely elongated spermatozoa of Drosophila hydei.
A,Reference number: S51364; MUID:95045538; PMID:7957199
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
                                                                                                                                                                                                                                                                                                           RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sperm tail-specific protein met101(2) - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
C;Date: 19-Jull-1996 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C;Accession: S51364; S34154
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A; Accession: $34154
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;Keywords: chromosomal protein; DNA binding; embryo; nucleosome; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: GB:M20314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               662 KETAEKKKCEKAAKKRKEAAEKKKCAEAAKKEKEAAEKKKCEEAA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
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61.9%;
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Pred. No. 0.41;
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                                                                                                                                                                               A;Cross-references: GB:M58563; NID:g155066; PIDN:AAA27480.1; PID:g155067 A;Note: the authors translated the codon TTC for residue 316 as Tyr, and
                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-384 < YEL>
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Query Match

Match 40.6%; Local Similarity 54.5%;

Conservative

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13;

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Score 86.5; Pred. No. 0. Mismatches 0.32;

DB 2; Length 384;

and CGA for residu

membrane protein

Matches

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R;Yelton, D.B.; Limberger, R.J.; Curci, K.; Malinosky-Rummell, F.; Slivienski, L.; Scho Infect. Immun. 59, 3685-3693, 1991
A;Title: Treponema phagedenis encodes and expresses homologs of the Treponema pallidum A;Reference number: A43592; MUID:91372983; PMID:1894368
A;Accession: B43592
                                                                                                                                                                               C;Species: Treponema phagedenis
C;Date: 30-Jan-1993 #sequence_revision 12-Mar-1993 #text_change 08-Oct-1999
C;Accession: B43592
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: B87553
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A; Status: preliminary
                                                                                                                                                                                                                                                                       outer membrane protein ImpB - Treponema phagedenis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: bacterial type I DNA topoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE005673; NID:g13423998; PIDN:AAK24422.1; GSPDB:GN00148
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A; Residues: 1-899 <STO>
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C;Accession: B87553
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C;Superfamily: histone H1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 АККҮАККАКАЕКАК-КАУКААЕАККААКҮЕКАААЕКАААКЕААҮЕА 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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55.6%;
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Pred. No. 0.45;
5; Mismatches
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3 0

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mst101-1 protein - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: 834153
R;Stover, C.K.; Pham, X.Q.; Brwin, A.L.; Mizoguchi, S.D.; Warrener, P.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; .; Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Neesen, J.; Heinlein, U.A.O.; Buenemann, H. submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70742
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F70742
                                                                          C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E83525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           834153
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                                                                                                                                                                                                                                                                                  밁
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C;Superfamily: neurofilament triplet H protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-344 < NEE >
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A; Accession: S34153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-199 < COL>
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                     E83525
TolA protein PA0971 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: FlyBase:Dhyd/mst101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X73480; NID:g313199; PID:g313200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                26;
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                                                                                                                                                                                                                                                                                  KEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAA 113
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Pred. No. 0.33;
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Pred. No.
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K.; Lim,
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Search completed: April 20, Job time: 8.88961 secs

2004, 23:18:23

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histone H1 homolog - Bordetella pertussis
()Species: Bordetella pertussis
()Species: Bordetella pertussis
()Date: 23-Jul-1996 #sequence_revision 06-Sep-1996 #text_change 24-Nov-1999
()Accession: S61926; S69327
R;Scarlato, V.; Arico, B.; Goyard, S.; Ricci, S.; Manetti, R.; Prugnola, A.; Manetti, R. Mol. Microbiol. 15, 871-881, 1995
Mol. Microbiol. 15, 871-881, 1995
A;Title: A novel chromatin-forming histone H1 homologue is encoded by a dispensable and A;Reference number: S61926; MUID:95319329; PMID:7596289
A;Accession: S61926
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A;Experimental source: strain PAO1
C;Genetics:
멼
                                                                                                                                                       A;Gene: bpH1
C;Superfamily: histone H1
                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 'X', 3-39 < SCA2>
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S61926
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A;Molecule type: DNA
A;Residues: 1-347 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
                                 Ś
                                                                                                                                                                                                                                                       A;Cross-references: EMBL:L37438; NID:g777717; PIDN:AAB59120.1; PID:g777718
A;Accession: S69327
                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-182 <S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: tolA; PA0971
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                                                                             Matches
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58
                                     27;
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                                                                                              Similarity
Conservative
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51.1%;
                                                                                            39.9%;
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Pred. No.
                                                                                            Score 85; DB 2;
Pred. No. 0.25;
                                                                             Mismatches
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5
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                                                                                                                 Length 182;
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Sequence 13743, A
Sequence 5390, App
Sequence 33, Appl
Sequence 13, Appl
Sequence 15, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 4, Appl
Sequence 2, Appl
Sequence 17, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 11, Appl

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Post-processing: Minimum Match 0% Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq length: 0
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213
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       Issued Patents AA:*
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/cgm2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgm2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgm2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgm2_6/ptodata/2/iaa/bcTUS_COMB.pep:*
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                                                                                          US-09-417-264-27

US-09-252-991A-29581

US-09-252-991A-2957

US-09-107-532A-5094

US-09-107-532A-5094

US-09-041-889-39

US-09-417-264-39

US-09-417-264-38

US-09-417-264-40

US-09-417-264-40

US-09-417-264-40

US-09-417-264-40

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US-09-417-264-40

US-09-417-264-40

US-09-417-264-40
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US-09-405-743A-7
US-09-405-743A-5
US-09-405-743A-6
US-09-405-743A-6
US-09-405-743A-1
US-09-405-743A-1
US-09-405-743A-1
US-09-489-039A-13565
US-09-489-039A-13565
US-09-05-426-201
US-09-05-426-201
US-09-041-889-27
US-09-041-889-27
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                      Sequence 2, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 201, App
Sequence 201, App
Sequence 27, Appl
Sequence 27, Appl
Sequence 29581, A
Sequence 29581, A
Sequence 304, Appl
Sequence 309, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 40, Appl
Sequence 30, Appl
Sequence 31, Appl
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Sequence
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SEQ ID NO 2
LENGTH: 45
TYPE: PRT
ORGANISM: Artificial Sequence
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; OTHER INFORMATION:
US-09-405-743A-2
; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: PEPTIDE . US-09-405-743A-7
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US-09-405-743A-7
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; Patent No. 6514938
; Patent INFORMATION:
GENERAL INF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-405-743A-2
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                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 199-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                  SOFTWARE:
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09405743A Patent No. 6514938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-09-543-681A-5390
US-08-529-055-33
US-08-714-741-32
US-08-152-488-13
US-08-303-025-15
US-08-436-703B-2
US-08-436-703B-2
US-08-436-703B-2
US-08-252-991A-22853
US-08-152-488-11
US-08-152-488-11
US-08-152-488-11
US-08-303-025-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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Pred. No. 1.4e-16;
; Mismatches 0;
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Length 45; Indels

0

Gaps

0

SYNTHETIC

SYNTHETIC

Result

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Score

131 126.5 120.5 108 95 91

81.5 78 77.5 77

86 11.5

89.5 89.5

134.5

Minimum DB Maximum DB

Scoring table: Perfect score: Sequence:

Title:

Run on:

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US-09-405-743A-5
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US-09-405-743A-3
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                                                                                                                                                                                                                                                                                SOFTWARE: P
SEQ ID NO 5
LENGTH: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence 3, Application US/09405743A Patent No. 6514938 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09405743A Patent No. 6514938
GENERAL INFORMATION:
                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                         Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
                                                                                                                                                                                                    OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 56
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                                                                        Local
1
                            30 -KAAAEKAAAKEAAYEA 45
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                                                                                                                                                                                                                                                                                                                PatentIn Ver. 2.1
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YKAEAAKAAKEAAYEA 77
                                                          AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKABAKY-KAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKKYAKAAKAE--KKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
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                                                                                                                                                                                                      Description of Artificial Sequence: PEPTIDE
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                                                                                                                                      50.6%;
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                                                                                                                         <u>.</u>
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                                                                                                                                      Score 131; DB 4;
Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 134.5; DB 4; Length 56; Pred. No. 4.1e-08;
                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                         6; Indels
                                                                                                                                                     Length 77;
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                                                            US-09-405-743A-1
                                                                            RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: P.
SEQ ID NO 4
LENGTH: 66
                    Sequence 1, Application US/09405743A Patent No. 6514938
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09405743A Patent No. 6514938 GENERAL INFORMATION:
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09405743A Patent No. 6514938
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
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TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 86
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE
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                                                                                                                                                                                                                                Local Similarity
                                                                                                                                     29 AKKYAKAAKAE--KKEYAAAEAK----YKAEAAKAAAKEAAYEA
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                                                                                                                                                                                                                             56.6%;
71.1%;
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45.3%; Pred. No. 4.6
                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                           Score 120.5; DB 4
Pred. No. 1.5e-06;
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                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
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APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A

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; Sequence 13565, Application US/09489039A
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PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13565
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 201, Application US/09095855 Patent No. 6160093 GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gary Breton et. al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 199-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 469
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                       APPLICANT: Tan, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and Methods for
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
NUMBER OF SEQUENCES: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 35
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                           STREET: Zovi -
                                                                    COUNTRY: U
ZIP: 98121
                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 AAEAQKKAEAAAAKKAQQEAEKKAQQEAAKQAAAEKAAAEKAAAQKA 292
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                                                                                                                  WA
                                                                                                                                                          E: Law Offices of Ann W. Speckman
2601 Elliott Avenue, Suite 4185
                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Tan, Paul L. J.

APPLICANT: Tan, Paul L. J.

ITILE OF INVENTION: Compounds and Methods for Treatment and TITLE OF INVENTION: Diagnosis of Mycobacterial Infections FILE REFERNCE: 11000.1002c4

CURRENT APPLICATION NUMBER: US/09/205,426

CURRENT FILING DATE: 1998-12-04

EARLIER APPLICATION NUMBER: 09/095,855

EARLIER FILING DATE: 1998-66-11

EARLIER APPLICATION NUMBER: 08/997,362

EARLIER APPLICATION NUMBER: 08/997,362

EARLIER APPLICATION NUMBER: 08/97,362

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1998-08-29

NUMBER OF SEQ ID NOS: 208

SOFTMARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                US-09-205-426-201
                                                                                                                                                                                               SEQ ID NO 201
LENGTH: 223
Query Match 42.7%; Score 91; DB 4; Length 223; Best Local Similarity 59.6%; Pred, No. 0.0074; Length 223; Matches 28; Conservative 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 201, Application US/09205426 Patent No. 6406704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acid
                                                                                                                                     ORGANISM: Mycobacterium vaccae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEPAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: F88tSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-UN-1997
APPLICATION NUMBER: 08/997,362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 223 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adough A2.7%; Score 91; DB 3; Length 223; Local Similarity 59.6%; Pred. No. 0.0074; Les 28; Conservative 5; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 АККУА-ККАКАБКАККАУКААЕАККААКУЕКАА-АЕКАААКЕААУЕА 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS: single
linear
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TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-041-889-27
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US-09-417-264-27
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CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/837,058
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: P-PM 3006
                                                                   GENERAL INFORMATION:

APPLICANT: Chary, Offer

TITLE OF INVENTION: Diagnosis, Prevention and Treatment of

TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using

TITLE OF INVENTION: Microbial UC pANCA antigens

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

ADDRESSEE: Campbell & Flores LLP

ADDRESSEE: Campbell & Flores LLP

ADDRESSEE: Campbell & Flores LLP
                                                                                                                                                                                                                                                                                            Sequence 27, Application US/09417264
Patent No. 6537768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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Patent No. 6033864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
STREET: 45.7
STREET: 45.7
CITY: San Diego
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Braun, Jonathan APPLICANT: Cohavy, Offer TITLE OF INVENTION: Diagnos TITLE OF INVENTION: Microbi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 4370 La Jo
CITY: San Diego
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  111 AKKVAKKAPAKKATKAAKKAATKAPA---RKAATKAPAKKAATKA 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKAKKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09041889
                                                                4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.0%;
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Ulcerative Colitis, and Clinical Subtypes Thereof, Using
Microbial UC pANCA antigens
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              RESULT 14
US-09-114-000C-5990
; Sequence 5990, Application US/09134000C
; Patent No. 6617156
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                                                                                                                                                                                                                                                                                                                                          US-09-252-991A-29581
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Patent No. 6551795
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 29581
                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR TILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 40
                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-F
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acid
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 214 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/417,264
                                                                                                                                                           185 AQKAAEAKKADEAKKAAEAKAAEQKKQADIAKKRAEDEAKKKAAEDA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 AKKVAKKAPAKKATKAAKKAATKAPA---RKAATKAPAKKAATKA 152
                                                                                                                                                                                                 1 АККҮАККАКАЕКАККА--ҮКААБАККААКҮЕКАААЕКАААКБААҮБА 45
                                                                                                                                                                                                                                                    24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
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                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                    40.4%; Score 86; DB 4; Length 407; 51.1%; Pred. No. 0.047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.0%; Score 89.5; DB 4; Length 214; 55.6%; Pred. No. 0.01; ative 4; Mismatches 13; Indels :
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US-09-252-991A-32957
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Search completed: April 20, 2004, 23:19:07 Job time : 9.35065 secs
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                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32957
LENGTH: 316
TYPE: PRI
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: LYAIN DOUGETTE-Stamm et al
APPLICANT: LYAIN DOUGETTE ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: 032796-032
CURRENT FILIG DATE: 1998-08-13
FRIOR APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOUTWARE: Patentin version 3.1
SEQ ID NO 5990
LENGTH: 497
TYPE: DET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32957, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                   Query Match 36.6%; Score 78; DB 4; Length 316; Best Local Similarity 54.8%; Pred. No. 0.26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 38.3%; Score 81.5; DB 4; Length 497; Local Similarity 47.1%; Pred. No. 0.17; Nes 24; Conservative 7; Mismatches 13; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 KKEAEKRIAEEQARQRAAAKKAEEQAAAQAQAAAQKAAABQAKATKAANBA 286
                                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 АККУАККАКАЕКАККАУКАЛЕАККААКУЕКАЛАЕКАЛАКЕЛА 42
                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                           19; Indels
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Title:
Perfect score:
Sequence:
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  Database :
                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                        Scoring table:
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                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                          141681 seqs, 52070155 residues
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213
1 AKKYAKKAKAEKAKKAYKAA.....AKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                        April 20, 2004, 23:08:59 ; Search time 6.13636 Seconds (without alignments) 381.848 Million cell updates/sec
SwissProt_42:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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triticum a	P40263 glyptotendi	klebsiella		P08286 gallus gall	P50887 drosophila	P37218 lycopersico	glyptoten	chironomu	3	chironomu		oncorhynch	salmo trut	streptomy	chironomu	parechinus	3 corynebact	_	5 drosophila	2 mycobacte	orynebact	0	5 drosophila	9 mycobacter	mycobacter	strongyloc	5 mycobact	drosophila	9934 escheri	6144 lytechinu	Description	

45	44	43	42	41	40	39	38	37	36	35	34
73	73	73	74	74	74	74.5	74.5	74.5	75	75.5	75.5
34.3	34.3	34.3	34.7	34.7	34.7	35.0	35.0	35.0	35.2	35.4	35.4
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H11_CAEEL	H12 CAEEL	H2BI CHLRE	FAU DROME	ALGP_PSEAE	RS16_BIFLO	IF2P_YEAST	RS16 CAUCR	ASR_ENTCL	H12 MOUSE	RL14 HUMAN	RS16_BACTN
		P50565 chlamydomon		P15276 pseudomonas	Q8g7gl bifidobacte	P39730 saccharomyc		Q93mh6 enterobacte	P15864 mus musculu	P50914 homo sapien	Q9rq15 bacteroides

# ALIGNMENTS

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166 AKKAAKKPAKKAAKKAAKKAAKKAAKKAAKKAAKKAA 208	1 аккуаккакаек-аккаукааеаккааккекаааекааакеаа 42	Query Match 48.6%; Score 103.5; DB 1; Length 210; Best Local Similarity 65.1%; Pred. No. 0.0011; Matches 28; Conservative 3; Mismatches 11; Indels 1; Gaps 1;	Chromosomal protein; Nuclear protein; DNA-binding; Multigene family. SEQUENCE 210 AA; 21746 MW; 08C38F64894007E2 CRC64;	SM00526; H15; 1.	PRINTS; PRO0624; HISTONEH5.	5	InterPro: IPR003819; Histone H5.	InterPro; IPR005818; Histone H1/H5.	PIR; A25550; A25550. HSSP: P02259; 1HST.	; X04488; CAA28177.1;		requires a license agreement (See http://www.is	ified and this statement is not removed. Usage by and for commerc	by non-profit institutions as long as its conter	and the EMBL outstation	h a collaboratic		SIMILARITY:	nucleosome chains into higher order	-!- FUNCTION: Histones H1 are necessary for the condensation of	1000	"Comparison of the late HI histone genes of the sea urchins Lytechinus pictus and Strongelocentrotus purpuratus.":		MEDLINE=87040778; PubMed=3022245;	TISSUE=Embryo;	CEDITATION OF PROPERTY OF THE	rcBI_TaxID=7653;	chinus.	, Euechi	Metazoa: Echinodermata; El	Lytechinus pictus (Painted sea uychin)	(Rel. 38, Last annotati	1988 (Rel. 06, Last	-1988 (Rel.	HI LYTEI STANDARD; PRT; 210 AA.	BI T

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RESULT 2
TOLA_ECOLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                             Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A.; "Filamentous phage infection: crystal structure of g3p in complex with its coreceptor, the C-terminal domain of TolA."; Structure 7:711-722(1999).
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91296736; PubMed=2068069;
Levengood S.K., Beyer W.F. Jr., Webster R.E.;
"Tolk: a membrane protein involved in colicin
extended helical region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90078104; PubMed=2687247; Levengood S.K., Webster R.E.; "Nucleotide sequences of the tolA and tolB genes and localization their products, components of a multistep translocation system in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tola protein.
Tola OR CIM OR EXCC OR LKY OR B0739
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10-OCT-2003 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97061202; PubMed=8905232;
                                                                                                                                                                                  MEDLINE=99332679; PubMed=10404600;
                                                                                                                                                                                                  (-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 298-421.
                                                                                                                                                                                                                                                  'TolA central domain interacts with Escherichia coli porins.";
                                                                                                                                                                                                                                                                    loubes R.;
                                                                                                                                                                                                                                                                                 Derouiche R., Gavioli M.,
                                                                                                                                                                                                                                                                                                        MEDLINE=97
                                                                                                                                                                                                                                                                                                                     NTERACTION WITH PORINS
                                                                                                                                                                                                                                                                                                                                                       roc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriol. 171:6600-6609(1989).
            BINDING TO THE BACTERIA. ALSO INVOLVED IN THE TRANSLOCATION OF BACTERIOPHAGE DNA.
SUBUNIT: INTERACTS, VIA DOMAIN II, WITH PORINS OMPC, OMPC, PHOE
                                                              FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF GROUP; COLICINS (COLICINS A, E1, E2, E3, AND K). NECESSARY FOR THE COLICINS TO REACH THEIR RESPECTIVE TARGETS AFTER INITIAL
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                                                                                                                                                                                                                                                                                                                                                       U.S.A. 88:5939-5943(1991)
                                                                                                                                                                                                                                                                                   Benedetti H., Prilipov A., Lazdunski C.,
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01-FEB-1995
01-FEB-1995
16-OCT-2001
                  Neesen J., Padmanabhan S., Buenemann H.;
"Tandemly arranged repeats of a novel highly charged 16-amino-acid motif representing the major component of the sperm-tail-specific axoneme-associated protein family Dhmst101 form extended alpha-helical rods within the extremely elongated spermatozoa of
                                                                                                                                                                                                                                                                                                                                                                                                                                             TURN
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                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                    SEQUENCE FROM N.A., AND CHARACTERIZATION. MEDLINE=95045538; PubMed=7957199;
                                                                                                                                                                                          MST101(2).
                                                                                                                                                                                                     Axoneme-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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             Drоворhila hydei.
                                                                                                  SEQUENCE FROM N.A.,
                                                                                                                                                                           Drosophila hydei (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
                                                                                                                        NCBI_TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
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 J. Biochem.
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                                                                                                                                                                                                                                                                                                                                                       Protein transport;
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(Rel. 31, Last sequence update)
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225:1089-1095(1994).
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Pred. No. 0.0068;
2; Mismatches
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DOMAIN II (ALPHA-HELICAL).

DOMAIN III (FUNCTIONAL).

10 X TANDEM REPEATS OF [ED]-K(1,2)-
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CYTOPLASMIC (POTENTIAL).
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Best Local
                                                                                                                                                                                                                                                           smegmatis.";
mol. Gen. Genet
-!- FUNCTION: F
                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                          MEDLINE=99110209; PubMed=9894918;
Lee B.H., Murugasu-Oei B., Dick T.;
"Upregulation of a histone-like protein in dormant Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
HSSP; P02346; 1HUU
                                                                                                                                                                                               -i- FUNCTION: Histone-like DNA-binding protein which is capable of wrapping DNA to stabilize it, and thus to prevent its denaturation under extreme environmental conditions (By similarity).
-i- SIMILARITY: Belongs to the bacterial histone-like protein family.
                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 700084 / mc(2)155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium smegmatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUP OR HLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9ZHC5;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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GG:0005737; C:cytoplasm; IDA.
GG:0005198; F:structural molecule activity; IEP.
GG:000788; F:axoneme assembly; IEP.
GG:0007288; F:axoneme assembly; IEP.
xm; Repeat; Multigene family; Polymorphism.
xm; Repeat; Multigene family; Polymorphism.
332 1268 59 X 16 AA APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Possible structural role in the sperm tail.
SUBCELLULAR LOCATION: Cytoplasmic.
TISSUS SPECIFICITY: Testis. Primary spermatocytes and early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spermatids.

DOMAIN: The predominant structure is alpha-helical.

POLYMORPHISM: Length polymorphisms exist between different strains, most likely caused by length variations within the tandem
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                 AF068138; AAD13809.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              663 KETAEKKKCEKAAKKRKEAAEKKKCAEAAKKEKEAAEKKKCEEAA 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                    1391 AA; 159000 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 42, Last annotation update)
protein HU homolog (Histone-like protein) (Hlp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.3%;
57.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 90; DB 1
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [KR] -K-X-C-X-X-X-A-K-X-X-K-X-X-X-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1B2A368F30F48878 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
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Best Local S
Matches 29
   Matches
                     Best
                                    Query Match
                                                                                      Pfam; Přó0538; linker histone; I.
PRINTS; PR00624; HISTONEHS.
ProDom; PD000373; Linkerhist_N; 1.
SMART; SM00526; H15; 1.
Chromosomal reversi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H1B_STRPU STANDARD; P1
P15869;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last seque
15-JUL-1999 (Rel. 38, Last annot
Histone H1-beta, late embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SMO0411; BHL; I.

SMART; SMO0411; BHL; I.

PROSITE; PS00045; HISTONE_LIKE; 1.

DNA-binding; DNA condensation; Repeat.

DNA-binding; DNA condensation; Repeat.

DNA-binding; DNA condensation; Repeat.

DNA-binding; DNA condensation; Repeat.
                                                                      SEQUENCE
                                                                                                                                                                 EMBL; M20314; AAA30052.1; -.
PSR; A28100; A28100.
HSSP; P02259; 1HST.
InterPro; IPR005818; Histone_H1/H5.
InterPro; IPR005819; Histone_H5.
InterPro; IPR003216; Linkerhist_N.
Defan_DEPOGE 10.1216; Linkerhist_N.
                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                Mol. Cell. Biol. 8:1842-1844:113007.

-I- FUNCTION: Histones H1 are necessary for the condensation nucleosome chains into higher order structures.

-I- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strongylocentrotus purpuratus."; Mol. Cell. Biol. 8:1842-1844(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lai Z.-C., Childs G.;

"Characterization of the structure and transcriptional patterns of the gene encoding the late histone subtype H1-beta of the sea urch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPRO00119; Bac DNAbind.
Pfam; PF00216; Bac DNA binding; 1.
PRINTS; PR01727; DNABINDINGHU.
PRODOM; PD000945; Bac DNAbind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88246461;
Lai Z.-C., Childs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7668
                   Local
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   26;
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                                                                   l protein;
211 AA; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 AA; 21230 MW;
   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=2837660;
                                                                   ; Nuclear protein; DNA-binding; Multigene 22169 MW; 9F214581334BBE7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.0%;
                42.0%;
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                  Score 89.5; DB 1; Length Pred. No. 0.025;
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Pred. No. 0.025;
3; Mismatches
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   Mismatches
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 10; Indels
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Gaps
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SKKTTKKVKKPAAKKAKKPA-AKKAAK--KPAAKKPAAKKAA 177

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RESULT 6
DBH_MYCBO
                                                                      Query Match
Best Local S
Matches 25
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16-OCT-2001 (Rel. 40, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
DNA-binding protein HU homolog (Histone-like)
HUP OR HLP OR HUPB OR MDP1 OR MB3010C.
                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Dogett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G., "The complete genome sequence of Mycobacterium bovis.", Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).

-- FUNCTION: Histone-like DNA-binding protein which is capable of wrapping DNA to stabilize it, and thus to prevent its denaturation under extreme environmental conditions (By similarity).

-- I- SIMILARITY: Belongs to the bacterial histone-like protein family.
                                                                                                                                                                                               InterPro; IPRO00119; Bac DNAbind.
Pfam; PF00216; Bac DNA binding; 1.
PRINTS; PR01727; DNABINDINGHU.
PRODOm; PD000945; Bac DNAbind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prabhakar S., Tyagi J.S., Prasad H.K.; "HLPMt-A target for differentiation of M.tuberculosis and M.bovis."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                     DNA-binding; DNA condensation; DOMAIN 1 90 B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsumoto S., Yukitake H., Matsuo "Identification of a novel proteir from Mycobacterium.";
                                                                                                                                                                                     SMART; SM00411; BHL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium bovis
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                                                                                                                                                                                                                                                                                  Y18421; CAB46493.1; -. AB013441; BAA78330.1; -. BX248344; CAD96697.1; -.
                                                                                                                                                                                                                                                                  P02346; 1HUU.
                     Similarity
                                                                                                                              PS00045; HISTONE LIKE; 1.

ing; DNA condensation; Repeat; Complete proteome.

BACTERIAL HISTONE-LIKE DOWAIN.
                                                                    101
137
208
214 AA;
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     Conservative
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                                                                    214 D
145 M
208 T
22187 MW;
                 42.0%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Camus J.-C., Medina N., Mansoor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein generating
   4.
                                                                                DEGENERATE REPEATS
MISSING (IN REF. 1)
T -> A (IN REF. 1)
                   Score 89.5;
Pred. No. 0.
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                                                                    CB09AF20FB353544
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T., Mineda T., Yamada T.;
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                                 DB 1; Length 214;
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                                                                                                  TS REGION.
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   Indels
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                            EMBL; Z83018; CAB05427.1; -. EMBL; AB007127; AAK47393.1; - PIR; G70673; G70673. HSSP; P02346; 1HUU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: Histone-like DNA-binding protein which is capable of
wrapping DNA to stabilize it, and thus to prevent its denaturation
under extreme environmental conditions (By similarity).
-!- SIMILARITY: Belongs to the bacterial histone-like protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (DEC-1997) to Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Savita P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 71-86, AND DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prasad H.K., Annapurna P.S., Dey A.B., Tyagi J.S., Jain N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .aboratory strains."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriol. 184:5479-5490(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Н
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TubercuList; Rv2986c; -. InterPro; IPR000119; Bac

PF00216; Bac\_DNA

ac\_DNAbind. \_binding; 1.

TIGR; MT3064;

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                                                         Matches
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Best Local
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Best Local !
                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIJINE-99372678; PubMed=10445506; Neesen J., Heinlein U.A.O., Heinz Glatzer K., Buenemann H.; Neesen J., Heinlein U.A.O., Heinz Glatzer K., Buenemann H.; "Proteins with tandemly arranged repeats of a highly charged 16-amino-acid motif encoded by the Dhmst101 gene family are structural components of the outer sheath of the extremely elongated sperm tails of Drosophila hydel."; Dev. Growth Differ, 41:93-99(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00045; HISTONE_LIKE; 1.

DNA-binding; DNA condensation; Repeat; Complete proteome.

DOMAIN 1 90 BOTTERIAL HISTONE-LIKE DOMAIN.

DOMAIN 101 214 DEGENERATE REPEATS REGION.

SEQUENCE 214 AA; 22187 MW; CB09AF20FB353544 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01727; DNABINDINGHU.
ProDom; PD000945; Bac DNAbind;
SMART; SM00411; BHL; T.
PROSITE; PS00045; HISTONE_LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Axoneme-associated protein mst101(3).
MST101(3) OR DHMST101.
Drosophila hydei (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DROHY
                                                                                                                                                                                                                                                                                                                                                                                               -!- TISSUE SPECIFICITY: Testis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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10-OCT-2003 (Rel.
10-OCT-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         001395;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7224;
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                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
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                                                                         Similarity
AKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAA 103
                           AKKAKAEKAKKAYKAAEAKK---AAKYEKAAAEKAAAKEAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKKVAKKAPAKKATKAAKKAATKAPA---RKAATKAPAKKAATKA 152
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42, Last sequence update)
42, Last annotation update)
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55.6%;
                                                                       41.5%;
61.0%;
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                                                                       Score 88.5; DB Pred. No. 0.039;
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                                                                                  DB 1;
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                                                                                   Length 275;
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RESULT 9
TMPB_TREPH
Query Match
Best Local
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REPEAT
REPEAT
REPEAT
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REPEAT
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-I- FUNCTION: TMP MAY SERVE AS A PORIN OR TRANSPORT PROTEIN FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treponema phagedenis.
Bacteria; Spirochaetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993
01-APR-1993
                                                                                                                                                                                                                                                                                                                                 DOMAIN
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PIR; B43592; B43592.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Kazan 5;
MEDLINE=91372983; PubMed=1894368;
                                                      REPEAT
                                                                                                 REPEAT
                                                                                                                      DOMAIN
                                                                                                                                                      REPEAT
                                                                                                                                                                            REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treponemal membrane protein B precursor (Antigen tmpB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Outer membrane-associated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LARGE MOLECULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TREPH
                                                                                                                                                                                                                                                                                                                                                                 Outer
                                                                                                                                                                                                                                                                                                                                                                            IPR008941; TPR-like
                                 AA,
                                                                                                                                                                                                                                                                                                                                                       membrane; Repeat; Signal.
L 21 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                      160
165
                                                     2543
270
279
                                                                                                                     42677 MW;
40.6%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spirochaetales; Spirochaetaceae; Treponema.
                                                                                                           6 X 8
A-A-E.
Score 86.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                               TREPONEMAL MEMBRANE PROTEIN
17 X 5 AA TANDEM REPEATS OF
                                                                                                                                                                                                                                                                                                                      [ED].
                                6E94CBC74294DE8C CRC64;
                                                                                                                      AA TANDEM REPEATS OF [EA] -A-A-R-X-
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 5; DB 1;
0.083;
          Length 384;
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K-A-A- [AKR] -
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Matches

Similarity

Conservative

6

Mismatches

Indels

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RESULT 11
    RESULT 10
RS16_CORES
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Best Local
                                                                           Q11142; 085733;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Heparin-binding hemagglutinin (Adhesin).
HEHA OR RV0475 OR MT0493 OR MTCY20G9.01 OR MB0485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Corynebacterineae; Mycobacteriaceae; Mycobacterium NCBI_TaxID=1773, 1765;
                                               Mycobacterium tuberculosis, Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                       Ribosomal protein; SEQUENCE 168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00886; Ribosomal S16; 1.
ProDom; PD003791; Ribosomal S16; 1.
TIGREAMS; TIGR00002; S16; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP005220; BAC18770.1; -. HAMAP; MF_00385; -; 1. InterPro; IPR000307; Ribosomal_S16.
                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                        нвна Мусти
                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGR00002; S16; 1.
PROSITE; PS00732; RIBOSOMAL_S16; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22723752; PubMed=12840036;
Nishio Y., Nakamura Y., Kawarabayasi )
Sugimoto S., Matsui K., Yamagishi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 efficiens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8FP30;
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                replacements responsible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium efficiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the S16P family of ribosomal proteins.
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                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                 EAITEKKKKAREEKEAKEAA--EKAAAEKAAAAEA 152
                                                                                                                                                                                                                                                                             KAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEA 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 42, Created)
(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
al protein S16.
                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                       Complete proteome 18228 MW; 443CE
                                                                                                                                                                                                                                                                                                                           40.4%;
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ble for the thermostability of Corynebacter:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawarabayasi Y., Usuda Y.,
Yamagishi A., Kikuchi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinobacteridae; Actinomycetales; bacteriaceae; Corynebacterium.
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                                                               and
                                                                                                                                                                                                                                                                                                                           Score 86; I
Pred. No. 0.
                                                                                                                                                                      PRT;
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                                                                                                                                                                      198 AA
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0.045;
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[1]
SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
SECIES-M.tuberculosis, and M.bovis;
STRAIN-H37Rv, ATCC 201 / H37Ra, and BCG / Paris 1173 P2;
STRAINE-98445421; PubMed-9770536;
MEDILINE-98445421; PubMed-9770536;
Menozzi F.D., Bischoff R., Fort E., Brennan M.J., Locht C.;
"Molecular characterization of the mycobacterial heparin-binding hemagglutinin, a mycobacterial adhesin.";
Proc. Natl. Acad. Sci. U.S.A. 95:12625-12630(1998).
                                                                                                                                                                                                                                                                                                                                           SPECIES=M.bovis; STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.
Harris B., Atkin R., Dogett J., Mayes R., Keating L., Wheeler P.,
Parkhill J., Barrell B.G., Cole S.T., Gory S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skellon S., Squares S., Squares R., Sulston J.B., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Menozzi F.D., Rouse J.H., Alavi M., Laude-Sharp M., Muller J.,
Bischoff R., Brennan M.J., Locht C.;
"Identification of a heparin-binding hemagglutinin present in
                                                                                                                                   "The heparin-binding haemagglutinin of M. tuberculosis is required extrapulmonary dissemination.";
Nature 412:190-194(2001).
                                                                                                                                                                                                     Pethe K., Alc
Menozzi F.D.;
                                                                                                                                                                                                                                        STRAIN=103, and B
MEDLINE=21342355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=M.tuberculosis, and M. STRAIN=ATCC 201 / H37Ra, and B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  SPECIES=M.tuberculosis, and M.bovis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97188915; PubMed=9064359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-16, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=M.tuberculosis; STRAIN=H3
MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriol. 184:5479-5490(2002).
             FUNCTION: REQUIRED FOR EXTRAPULMONARY DISSEMINATION. MEDIATE ADHERENCE TO EPITHELIAL CELLS BY BINDING TO SULFATED GLYCOCONJUGATES PRESENT AT THE SURFACE OF THESE CELLS; BINDS HEPARIN, DEXTRAN SULFATE, FUCCIDAN AND CHONDROITIN SULFATE PROMOTES HEMAGGLUTINATION OF ERYTHROCYTES OF CERTAIN HOST SPINDUCES MYCOBACTERIAL AGGREGATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Med. 184:993-1001(1996).
                                                                                                                                                                                                                      Alonso S.,
                                                                                                                                                                                                                                                                and BCG;
                                                                                                                                                                                                                                            PubMed=11449276;
                                                                                                                                                                                                                      Biet F., Delogu G., Brennan M.J., Locht C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and M.bovis;
and BCG / Paris 1173 P2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Churcher C.,
                                       HOST SPECIES
                                                                                                                      MEDIATES
                                                                                                                                                                                                                                                                                                                                                                                                                                Simon S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S.,
                                                                                                                                                                                 for
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SUBCELLULAR LOCATION: Surface-associated

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MST1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Arthropoda, Hexapoda, Inss
Neoptera, Endopterygota, Diptera, Brachycera,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                    MST1_DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                repetitive, axoneme-associated protein with Y chromosomal deletion mutant flies.", Dev. Biol. 162:414-425(1994).
                                                                                                                                               Neesen J., Buenemann H., Heinlein U.A.O.; "The Drosophila hydei gene Dhmst101(1) encodes a testis-specific,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF074390; AAC26052.1; -. EMBL; Z77162; CAB00936.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                    Drosophila hydei (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                  Axoneme-associated protein mst101(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---
                                                                                                                                                                                  MEDLINE=94200512; PubMed=8150205;
                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                 NCBI_TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DROHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TubercuList; Rv0475; -
FUNCTION: Possible structural role in the sperm tail. associated with axonemal structures. SUBCELLULAR LOCATION: Cytoplasmic (By similarity). TISSUE SPECIFICITY: Testis. Located in spermatocytes spermatid bundles.

DOMAIN: The predominant structure is alpha-helical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: SERUM FROM PATIENTS DIAGNOSED WITH ACTIVE TUBERCULOSIS THAT HAD NOT BEEN VACCINATED CONTAINS ANTIBODIES T RECOGNIZE HEHA, WHEREAS SERUM FROM HEALTHY INDIVIDUALS DOES NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: HEPARIN BINDING SEEMS TO REQUIRE THE C-TERMINAL END DOMAIN OF HEHA. PROGRESSIVE TRUNCATIONS FROM THE C-TERMINAL END DIMINISH THE AFFINITY FOR HEPARIN.

PTM: GLYCOSYLATED. GLYCOSYLATION MAY PROTECT THE PROTEIN FROM PROTEOLYTIC DEGRADATION AND BE IMPORTANT FOR HEMAGGLUTINATION. I SUGGEST'S THAT THE CARROHYDRATE MOIETY MAY BE LOCATED WITHIN THE TERMINAL DOMAIN OF HEHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: STRONG, TO M.LEPRAE HBHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONTAIN ANY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F70742; F70742
                                                                                                                                                                                                                                                                                                                                                                                                                                      DROHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adhesion; Heparin-binding; Hemagglutinin; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z77162; CAB00936.1; -.
AE006951; AAK44716.1; ALT_INIT
BX248335; CAD93348.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 EKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKAAPAKKAAPAKKAAPAKKAPAKKAA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151
120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21403 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALA/LYS-RICH.
R -> P (IN REF. 1).
; 513760F6F1EB6042 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 86; DB 1;
Pred. No. 0.052;
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                 Insecta; Pterygota;
                                                                                                                                   differential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                  sperm tail.
                                                                                                                                                                                                                                                                                    Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                              abundance
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RESULT 13
TOLA_PSEA
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Best Local S
Matches 26
                                                                         STRAIN=ATCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043;

Stover C.K.; Pham X.-Q.T.; Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Smith K.A., Spencer D.H., Hancock R.E.W., Lory S., Olson M.V.,

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen.";

Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P50600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                          -!- SUBCELLULÂR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                   Duan
                                                                                                                                                                                                                                                                                                                                 REVISIONS TO N-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa.";
J. Bacteriol. 178:7059-7068(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=PAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tola protein.
Tola OR PA0971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PlyBase; FBgn0011816; Dhyd\mst101(1).

GO; GO:0005737; C:cytoplasm; IDA.

GO; GO:0005198; F:structural molecule activity; IEP.

GO; GO:0007288; P:axoneme assembly; IEP.

Sperm; Repeat; Multigene family.

DOMAIN 58 337 19 x 16 AA APPROXIMATE
                                                                                                                                                                                                                                                                                                                                                                                               Dennis J.J., Lafontaine E.R., Sokol F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97113525; PubMed=8955385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOLA_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X73480; CAA51875.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -I- POLYMORPHISM: The number of repeats varies between strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eseudomonadaceae;
                                                 similarity.
                                                               FUNCTION: Involved in the tonB-independent
               (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S34153; S34153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                   Sokol P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37793 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence update) annotation updat
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Pred. No. 0.084;
3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 X 16 AA APPROXIMATE TANDEM REPEATS K-K-K-C-X-E-X-A-[KQ]-K-X-X-E-X-A-X.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sokol P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24C65D2510387E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 of the tolQRA genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 344;
                                                               uptake of
                                                               proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT 14
RS16_CORGI
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Best Local S
Matches 24
                  Best Local Similarity
                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bidinformatics and the EMBL outstation the European Bidinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                        TIGRANS; TIGRO0002; S16; 1.

PROSITE; PS00732; RIBOSOMAL_S16; FALSE_NEG.
Ribosomal protein; Complete proteome.
Ribosomal protein; Transplete proteome.
SEQUENCE 165 AA; 17837 MW; 61DD81961BC3
                                                                                                    InterPro; 1rkuvvvv 1816; 1.
Pfam; PF00886; Ribosomal_S16; 1.
ProDom; PD003791; Ribosomal_S16; 1.
                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.", Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the S16P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORGL
                                                                                                                                                       EMBL; AP005280; BAB99447.1; -. HAMAP; MF_00385; -; 1. InterPro; IPR000307; Ribosomal_S16.
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U39558; AAC44660.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8NNX3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPSP OR CGL2054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMÁIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR006260; TonB_C.
TIGRFAMs; TIGR01352; tonB_Cterm; l.
Transport; Protein transport; Transmembrane; Repeat; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                   Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; AE004530; AAG04360.1; -. E83525; E83525.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQKAAEAKKADEAKKAAEAKAAEQKKQADIAKKRAEDEAKKKAAEDA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     347 AA;
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 41, Created)
(Rel. 41, Last seq
(Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 41, Last sequence update)
protein S16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16
37
347
216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37935
             38.5%; Score 82; DB 1. 62.9%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.4%;
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 4; Mismatches
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P02256;
21-JUL-1986
21-JUL-1986
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Eur. J. Biochem. 104:559-566(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-84.
MEDLINE=80156831; PubMed=6767609;
Strickland W.N., Strickland M., de Groot P.C., von Holt C.,
                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                    PRINTS; PR00624; HISTŌNEH5.
ProDom; PD000373; Linkerhist_N; 1.
SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                             InterPro; IPR005818; Histone_H1/H5
InterPro; IPR005819; Histone_H5.
InterPro; IPR005316; LinkerNist N.
Pfam; PF00538; linker_histone; I.
                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the histone
PIR; A91090; HSURIP.
                                                                                                                                                                                                                                                                                                                                                                                                  -I- FUNCTION: Histones H1 are necessary for the condensation of nucleosome chains into higher order structures.
-I- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                              the entire primary structure.";
Eur. J. Biochem. 104:567-578(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 2. Sequence of the C-terminal CNBr peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strickland W.N., Strickland M., Brandt W.F., von Holt C., Lehmann A., Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parechinus angulosus (Angulate sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                            VARIANT
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Copyright (c) 1993 - 2004 Compugen Ltd.
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# SUMMARIES

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Q9nfp6 trypanosoma		Q84528 paramecium	Q8p6u0 xanthomonas	O94567 schizosacch		Q9s2m2 streptomyce	Q8myc3 mytilus cal	Q7ysz7 rhodnius pr	Q81hj4 bacillus ce		Q9cm70 pasteurella	Q9at18 lens culina			σ						Q45370 bordetella	Q7vut9 bordetella	Q8t9r3 leishmania		093946 candida alb	0 xanthor	Q8xvn7 ralstonia s	Q9a5j6 caulobacter

## ALIGNMENTS

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Query Match 50.9%; Score 108.5; DB 16; Length 379; Beat Local Similarity 65.1%; Pred. No. 0.0043;

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Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
A. Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
A. Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
A. Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
A. Chillingworth T., Roble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
A. Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
A. Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
A. Rabbinowitsch E., Rutter S., Sanders M., Squares S., Stevens K.,
A. Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
A. Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
Comparative analysis of the genome sequences of Bordetella pertussis,
Bordetella parapertussis and Bordetella bronchiseptica.";
Nat. Genet. 35:32-40(2003).
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Best Local (
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                                                                                                                                                                                        MEDLINE=22735913; PubMed=12835416;
Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Gloeckner F.O., Kube M., Boxer M., Heitmann K., Rabus R.,
Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
Schlesner H., Amann R., Reinhardt R.;
"Complete genome sequence of the marine planctomycete Pirellula
    Hypothetical protein; SEQUENCE 461 AA; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Planctomycetaceae; Pireliula.
NCBI_TaxID=117;
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                                                                                                               n 1.";
Natl. Acad. Sci. U.S.A. 100:8298-8303(2003)
                                                                        BX294143; CAD74436.1; -
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Q8FJT1;
01-MAR-2003
01-MAR-2003
01-OCT-2003
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Escherichia coli 06.
             Tola protein.
Tola or C0818.
                                                                                                                                                                                                                                                                           Complete proteome. SEQUENCE 394 AA;
                                                                                                                                                                                                                                                                                                    EMBL; AB005252; AAG55075.1; -.
EMBL; AB002535; BAB34197.1; -.
FIR; F90725; F90725.
PIR; G85576; G85576.
                                                                                                                                                                                                                                                                                                                                                          Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Wasunaga T., "Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=0157:H7 / RIMD 0509952;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
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STRAIN=0157:H7 / E
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TOLA OR Z0907 OR ECS0774
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Pred. No. 0.
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Enterobacteriaceae; Escherichia. NCBI\_TaxID=217992;

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

SEQUENCE FROM N.A.

SOURCE REPRESENTATION OF THE PROPERTY OF THE P

STRANN-06:H1 / CFT073 / ATCC 700928;
MSDLINS-22388234; PubMed=12471157;
Welch R.A., Burland V., Flunkett G. III, Redford P., Roesch P.,
Welch R.A., Burland V., Flunkett G. III, Redford P., Stroud D.,
Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

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247 KKAAEKAAAEKAAADKKAAAEKAAADKKAAA-AKAAAEKAAAAKAAAEA 294

Q83SA1

PRELIMINARY;

413

8

01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigella.

Shigella flexneri.

TaxID=623

Membrane spanning protein, required for outer membrane integrity. TOLA OR SE0558 OR S0571.

Matches Query Match Best Local

32;

Conservative

2;

Mismatches

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Indels

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Similarity

46.0%;

Score 98; DB 16 Pred. No. 0.051;

DB 16; Length 421;

Complete proteome. SEQUENCE 421 AA;

421 AA;

43184 MW; DB296626F056D385 CRC64;

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RESULT 6
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STRAIN=24577 / ATCC 700930 / Serotype 2a;

STRAIN=24577 / ATCC 700930 / Serotype 2a;

MEDLINE=22590274; PubMed=12704152;

Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,

Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling

Mau B., Perria N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,

Schwartz D.C., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=2272406; FubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong v.
Yang J., Yang F., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence and comparative flexneri serotype 2a strain 2457T."; Infect. Immun. 71:2775-2786(2003).
                                                                                                                                                                                                                                                                                                           EMBL; AE015086; AAN42202.1; -.
EMBL; AE016979; AAP16075.1; -.
                                                                                                                                                                                                                                      SEQUENCE
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Pred. No. 0.099;
3; Mismatches
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RRA Baquero F., Brangeul L., Buchrieser C., Rusnick C., Amend A.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Battian K.-D., Feshi H., Garcia-del Portillo F., Garrido P.,
RETTIAN R.-D., Feshi H., Garcia-del Portillo F., Garrido P.,
RA Battiar L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maltournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
T. Science 294:849-852(2001).
REMEL, AL591981; CAD00019.1; -.
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Best Local
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                       MEDIINE=22608415; PubMed=12721630; Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kapatra, V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T., Chu L., Mazur M., Haselkorn R., Fonstein M., Ehrlich S.D., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., Overbeek R., Kyrpides N.;
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Q8Y5W4;
QHAR-2002 (TIEMBLIEL 20,
01-MAR-2002 (TIEMBLIEL 20,
01-JUN-2003 (TIEMBLIEL 24,
                                                                                                                                                                                                                                                                                                                         Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria; Firmicutes; Bacillales; Bacillaceae;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
TCdA-E operon negative regulator.
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01-JUN-2003
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Pfam; PF01476; LysM; 1.
SMART; SM00257; LysM; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 239 AA; 25836 MW; 72E59D576E0D7832 CRC64;
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GO; GO:0016998; P:cell wall
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Genome sequence of Bacillus cereus and comparative analysis with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 KAAAEKAEADKKKQEEDAVKAANAKKEQEAAEEKAAADKAAAEKAAAE 171
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   SEQUENCE (2) / M145;
STRAIN=38(2) / M145;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; Charles G... Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins
Harper D., Goble A., Hidalgo J., Hornsby T., Howarth
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence up
01-MAR-2003 (TREMBLREL. 23, Last annotation
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Mature 423:87-91(2003).
EMBL; AE017001; AAP07941.1; -.
Complete proteome.
SEQUENCE 248 AA; 27107 MW;
                                                                                                                                                                                                                                                                                            Streptomycineae;
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                            Streptomyces coelicolor.
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DNA Res. 9:189-197(2002).
EMBL; AP005962; BAC52804.1; -
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=USDA 110;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
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117 AA;
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Pred. No. 0.085;
4; Mismatches 9;
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922A67
Q92A67;
Q92A67;
Q92A67;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation updat
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A Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
A Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
Chillingworth T., Collins M., Basham D., Bason N., Cherevach I.,
Chillingworth T., Collins M., Basham D., Davis P., Doggett J.,
A Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
A Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
A Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
A Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
A Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,
Comparative analysis of the genome sequences of Bordetella pertussis,
Bordetella parapertussis and Bordetella bronchiseptica.",
IL Nat. Genet. 35:32-40(2003).
                                                                                          Matches
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BPH1 OR BPP3905.
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Nature 417:141-147(2002).
EMBL; AL939110; CAC28545.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=12822 / ATCC BAA-587;
MBDLINE=22827954; PubMed=12910271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella parapertussis.
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
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                                             5 AKKAKAEKAKK--AYKAAEAKKAAKYEKAAAEKAAAKEAAYE
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Similarity 60.5%;
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197 AA; 19583 MW;
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                                                                                        Conservative
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Last
                                                                                   Score 90.5; DB Pred. No. 0.13; 4; Mismatches
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Pred. No.
                                                                                                                                                                                 11D642F2BF5AE1EE CRC64;
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XX MEDIINE-21537279; pubmed-11679669;

XA Glaser P., Frangeul L., Buchrieser C., Rusnick C., Amend A.,

Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

ARA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Domann E., Dominguez-Bernal G., Duroud E., Durant L., Dussurget O.,

ARA Domann K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,

ARA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

ARA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

ARA Mordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

ARA Nordsiek G., Novella S., de Pablos B., Ferez-Diaz J.-C., Purcell R.,

ARA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

**Comparative genomics of Listeria species.";

Science 294:849-852(2001).

**Brigge B., Aliges B., Perez-Diaz J., Aliges B., Perez-Bar B.,

**Paratine genomics of Listeria species.";

Science 294:849-852(2001).
                                                                                             Matches
                                                                                                                  Query Match
Best Local
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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GO; GO:0016998; P:cell wall catabolism; IEA.
InterPro; IPR002482; LysM.
Pfam; PF01476; LysM; 1.
SMART; SM00257; LysM; 1.
                                                                                                                                                                                                                              tagging.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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Bacteria; Firmicutes;
NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
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SEQUENCE 243 AA; 25963 MW; 6B2493D143B159D1 CRC64;
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                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                           EMBL; AY089703; AAM09090.2; -.
                                                                                                                                                                                                                                                                                      "Mini-TnoprI, a new mini-transposon for in vivo protein epitope
                                                                                                                                                                                                                                                                                                                Kholti A., Plesa M.,
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=87883;
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    19
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                                          AKKVQPAKKAAAVKKVAAKKVAVKKVAAKKAAPAKKAAAKKVAAKKAA 66
                                                                                                                                                                               182 AA;
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                                                                                                                                                                               18768 MW;
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                                                                                        Score 89; DB:
Pred. No. 0.18
3; Mismatches
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Pred. No. 0.18;
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                                                                                                                                                                               243C5AECDA5A0234 CRC64;
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                                                                                                                                   DB 2;
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RESULT 15
Q88NI6
Q88NI
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DT 01-JU
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DE Biopo
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ID Q9WWX
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"Characterization of an Opt. null mutant of Pseudomonas putida.";

RT "Characterization of an Opt. null mutant of Pseudomonas putida.";

RL J. Bacteriol. 178:5836-5840(1996).

RMB1; X74218; CAB50780.1; -.

DR GO:0000786; C:nucleosome; IEA.

GO; GO:00005634; C:nucleosome; IEA.

GO; GO:0003677; F:NNA binding; IEA.

GO; GO:0003637; F:nucleosome assembly; IEA.

GO; GO:000334; P:nucleosome assembly; IEA.

RO; GO:000334; P:nucleosome assembly; IEA.

DR InterPro; IPR005819; Histone_H5.

DR InterPro; IPR006260; TonB_C.

DR PRINTS; PR00624; HISTONUBES.

DR TICRFAMS; TIGR01352; tonB_Cterm; 1.

SQ SEQUENCE 372 AA; 40113
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Best Local S
Matches 27
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01-NOV-1999
01-OCT-2003
                    Q88NI6, PRELIMINARY;
Q88NI6;
01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation updat Biopolymer transport protein TolA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96198174; PubMed=8626299;
Rodriguez-Herva J.J., Ramos-Gonzalez M.I., Ramos J.;
"The Pseudomonas putida peptidoglycan-associated outer membrane lipoprotein (PAL) is involved in maintenance of the integrity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas putida.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tolk protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rodriguez-Herva J.J.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
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                                                                                                                                                                                                                                                                                                                  ABDAAKAAEAAKAAEAKKAAEAKKADEAKKAAEKQQADIAKKKAEDEAKKKAEEEAKKAA 180
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3 (TrEMBLrel. 25,
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39.7%;
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| MW; 87F49785ECC3C0BC CRC64;
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Last annotation update)
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I Environ. Microbiol. 4:799-808(2002).

R EMBL; AB016778; AAN66845:1; -

R TIGR; PP1221; -

R GG; GO:0000786; C:nucleosome; IEA.

R GG; GO:0005634; C:nucleus; IEA.

R GG; GO:0005634; P:nucleus; IEA.

R GG; GO:0005634; P:nucleosome assembly; IEA.

R GG; GO:000534; P:nucleosome assembly; IEA.

R GG; GO:000534; P:nucleosome assembly; IEA.

R GG; GO:000534; P:nucleosome assembly; IEA.

R PRINTS; PR00624; HISTONEHS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22433060; PubMed=12534463;

Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,

Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,

Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,

Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,

Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,

Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,

Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,

Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome. SEQUENCE 372 AA; 40133 MW; 87F49785ECC3C0BC CRC64;
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Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                      181 AEEAKKKA 188
                                                                                                                                                                                                                                                                                                                                                                       121 AEDAAKAAEAAKAAEAKKAAEAKKADEAKKAAEKQQADIAKKKAEDEAKKKAEEEAKKAA 180
                                                                                                                                                                                                                                                                            38 AKEAAYEA 45
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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seq length: 2000000000
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1: geneseqp1980s:*
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213
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                       geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
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geneseqp2000s:*
geneseqp2001s:*
geneseqp2004s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	o.	ຫ	.4	ω	2	ь	No.	Result
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AAW43082	AAW44934	ABG28693	ABU40185	ABU36893	ABU34623	AAY57353	AAY34055	ABP70903	492	AAR06445	261	ABB49123	ABU31397	ABU28559	AAR28871	44	AAY82571	82	AAY82574	AAY82576	AAY82575	AAY82573	AAY82577	AY82	ID	
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45	44	43	42	41	40	9	38	37	36	35	34	u S	32	31	30	29	28	27	26
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Aay57365 Human his	ж	Abb60086 Drosophil		œ	Abb63276 Drosophil	Abo23523 Pseudomon	Abu26064 Protein e	Abu22879 Protein e	Abu33811 Protein e	Abu47123 Protein e	Abg71044 Tumour ne			Abu39221 Protein e	Aag70868 C albican	Aab20575 Mycobacte	Abj18771 Pseudomon	w	Aaw44936 Mycobacte

### ALIGNMENTS

#### RRESULT 1 AAY82572 ID AAY8 XX AAY8 AC AAAY8 AC AAAY8 AC AAAY8 AC CAPA AC AAY8 XX COPO DE COPO XW COPO XW Glab KW Gibb KW Gibb KW Gibb KW Hash Copolymer; molecular weight marker; TV-marker; immune disease; glatizamer acetate; autoimmune disease; antianthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyronimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Unidentified. Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:2. AAY82572; WO200018794-A1. AAY82572 standard; peptide; 45 pemphigus vulgaris; systemic lupus erythematosus. 28-JUL-2000 (first entry) 8

06-APR-2000.

24-SEP-1999; 99WO-US022402.

25-SEP-1998; 98US-0101693P.

(YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Gad A, Lis D;

WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

Claim 10; Page 14; 72pp; English.

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides

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RESULT 2
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Best Local (
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Claim 10; Page 14; 72pp; English
                                                       Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Corbin's disease, chronic immune thyroiditis, autoimmune uveoretinitis, Corbin's ensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200018794-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
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                                                                                                                                                      WPI; 2000-317499/27.
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                                                                                                                                                                                                                                                                                                                                                                   25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                              24-SEP-1999;
                                                                                                                                                                                                                                                                     (YEDA ) YEDA RES & DEV CO LTD.
(TEVA-) TEVA PHARM USA INC.
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Pred. No. 2.4e-16;
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                                                          of immune diseases.
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AAY82577 represent specifically claimed copolymer molecular

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases

WPI; 2000-317499/27

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(TEVA-) TEVA PHARM USA INC.
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Pred. No. 8.8e-08;
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RESULT 4
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Best Local !
                                                                                                                                                                                                                                                                                                                                        glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antityroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
                                                                                                                                                                                                                                                                                    Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 56 AA;
                 Gad A,
                                                                                                                                                                                                       06-APR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY82575 standard; peptide; 77 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Page 14; 72pp; English.
                                                                                                                      25-SEP-1998;
                                                                                                                                                             24-SEP-1999;
                                                                                                                                                                                                                                                                                                                           pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copolymer; molecular weight marker; TV-marker; immune disease;
                                                           (YEDA ) YEDA RES & DEV CO LTD (TEVA-) TEVA PHARM USA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39;
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                                                                                                                      98US-0101693P
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Lie D

24-SEP-1999;

99WO-US022402

06-APR-2000.

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RESULT 5
AAY82576
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Best Local
                                                                                                                                                                                          glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the respective of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 77 AA;
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                                                                                                                                 Unidentified.
                                                                                                                                                                                                                                                                                                                                                                              Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                           Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY82576 standard; peptide; 86 AA
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                                                                                      WO200018794-A1
                                                                                                                                                                          pemphigus vulgaris; systemic
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Pred. No. 3.6e-07;
0; Mismatches 6
                                                                                                                                                                            lupus erythematosus.
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Best Local
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           Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasshenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer accetate molecules, which makes them ideal for use as molecular weight markers
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  pemphigus vulgaris; systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 86 AA;
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                                                                                                                                                                                                                                         Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4.
                                                                                                                                                                                                                                                                                        28-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                           AAY82574 standard; peptide; 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-317499/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YKAEAAKKAYKAEAAKAAAKEAAYEA 86
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lupus erythematosus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 66 AA;
                                                                                 Antisense; prokaryotic essential
                                                                                                                      Protein encoded by Prokaryotic essential gene #13351.
                                                                                                                                                          19-JUN-2003
                                                                                                                                                                                            ABU27824;
                                                                                                                                                                                                                              ABU27824 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY82571 to AAY82577 represent specifically claimed copolymer molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
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(TEVA-) TEVA PHARM USA INC.
                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                        1 АККУАККАКАБКАККАУКААБАККААКУЕКАААБКАААКБААУБА 45
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                              protein; 428 AA
                                                                                                                                                                                                                                                                                                                                                                                                            56.6%;
71.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 120.5; DB 3
Pred. No. 4.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                   gene; cell proliferation; drug design
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                         6;
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                                                                                                                                                         The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression CC of the nucleic acid inhibits proliferation of a cell. Also included are: CC (1) a vector comprising a promoter operably linked to the nucleic acid (2) a host cell containing the vector; (3) an isolated cc encoding a polypeptide whose expression is inhibited by the antisense CC nucleic acid; (2) a host cell containing the vector; (3) an isolated cc polypeptide; (5) producing the polypeptide; (6) inhibited by the cc integration or the activity of a gene in an operor required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway CC required for proliferation, or that inhibits cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an CC compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits proliferation of collection of strains; or (13) identifying the target of a compound that inhibits the gene CC proliferation of an organism. The antisense nucleic acids are useful for clentifying proteins or screening for homologous nucleic acids required cfung discovery programs, or for screening homologous nucleic acids required cfung discovery programs, or for screening homologous nucleic acids of the target prokaryotic essential genes. Note: The squence is encoded by one of the target to the proliferation in cells other than S. aureus, S. typhimurium, contained the printed specification, but was obtained contained contained the printed specification, but was obtained contained the proper strained the printed specification, but was obtained 
                                                                               Matches
                                                                                                                Query Match
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25-OCT-2001;
08-FEB-2002;
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Wall
                                                                                                                                                       Sequence 428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2001;
                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                                                                                                Local
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  199
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                                                                           32;
                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELITRA PHARM INC.
Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 2001US-00815242.
; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002WO-US009107.
                                                                                            50.9%;
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Carr G
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                                                                     Score 108.5; DH b;
Pred. No. 0.00058;
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohlsen :
Forsyth !
                                                                                                              Length 428;
                                                                         Indels
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                                                                           11;
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Xu HH;
                                                                           Gaps
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RESULT 8

XXX

AAY82571

AAY82571 standard; peptide; 35

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-KEAKAKAAEAAAKEAAYEA 35

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RESULT 9

AAR06446

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                                                                                                                                           Query Match
Best Local (
                                                   Matches
                                                                                                                                                                             disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
                                                                                                                                                                                                                                                                                                                                                                                      AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides from the present invention are copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune uvecretinitis. Crohn's because disease include arthritic anaemia, autoimmune diseases and inflammatory conditions, autoimmune uvecretinitis. Crohn's
                                                                                                                                           Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antifilammatory; antidiabetic; thyronimetic; haemostatic; antipporiatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatod arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-317499/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gad A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200018794-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copolymer; molecular weight marker; TV-marker; immune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (YEDA ) YEDA RES & DEV CO LTD.
(TEVA-) TEVA PHARM USA INC.
    1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                      Similarity
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0101693P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US022402.
                                                                    50.7%;
                                                                    Score 108; DB 3
Pred. No. 5e-05;
                                              Mismatches
                                                                                            DB 3;
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                                                                                            Length 35;
                                                Indels
                                              10;
                                              Gaps
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RESULT 10
AAR28871
ID AAR28
XX
AC AAR28
XX
DT 25-MA
DT 23-MA
XX
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Best Local S
Matches 28
                                                                                                                                                                                                                                                                                       occurs between the Protein A and TCOP-1 sequences. A menchionine residue 5' linker sequence, in order that the COP-1 sequences, originating from the from the fusion protein. rCOP-1-19 contains oligonucleotide duplexes incoding the following segments: YKK, AAE, KAK, KKA, YEA, AKA KEA, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the fusion protein. The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in certain amino acids. See also AAQ05664. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-19 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US4691009, NRRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-plasmids encode fusion proteins. A methionine residue glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue
                 25-MAR-2003
23-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant copolymer 1-19, myelin basic protein analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
03-JAN-1991
                                                                                 AAR28871 standard; peptide; 46 AA.
                                                                                                                                                                                                                                                               Sequence 106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 12; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or immunological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-FEB-1989;
07-FEB-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP383620-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis; multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR06446;
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                                                                                                                                                                             3 КҮАККА-КАЕКАККАҮКААБАККААКҮЕКАААБКАА------АКБА 41
                                                                                                                                                                                                        Similarity 58.3
28; Conservative
                                                                                                                                                     KAAKKAYEAEKAKAKYEAKKAEKAEKAEKAAAEKKAKEAKKAEKAKEA 55
                (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89US-00312541.
90US-00473845.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; 106 AA.
                                                                                                                                                                                                                      46.7%;
58.3%;
                                                                                                                                                                                                        Score 99.5; DB 2; Length 106; Pred. No. 0.0013; Indels 4; Mismatches 7; Indels
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                           03-MAY-1991;
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                                                       01-MAY-1992;
                                                                                 12-NOV-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
    (UNIW ) UNIV WASHINGTON
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High affinity macrophage mannose receptor ligand compound #9.

glycopeptide; mannose; mannosylated; glycosylated; mannose receptor; macrophages, monocytes; destroy; cytotoxicity; label; image; alter; macrophage processing of antigen; MHC restriction; inflammation; inflammatory diseases; macrophage secretory products; Crohn's disease; legionnaires disease; mononuclear phagocytes; HIV; AIDS; lysosomal storage diseases; Gaucher's disease; asthma; alveolar macrophages metastasis; systemic macrophages; deliver; antigenic peptides; prevent transplant rejection; organ transplantatio antitumour agents; cancer; toxins. transplantation;

Location/Qualifiers

, p	/note= "opt glucosamine.	may Maj	may have . May also	mannose, have no	fucose interi	, glucose or fering substi	or N-AC- stits."
ied-site	note= "opt glucosamine.	may "	have	mannose,	fucose,	glucose	or N-Ac-
ied-sit	/note= "opt glucosamine.	may "	have	mannose,	fucose,	glucose	or N-Ac-
בי הם לי	ote= "opt ucosamine.	may "	have	mannose,	fucose,	glucose	or N-Ac-
1. E	/note= "opt glucosamine.	may "	have	mannose,	fucose,	glucose	or N-Ac-
ied-sit	"opt	may "	have	mannose,	fucose,	glucose	or N-Ac-
ed-site	<pre>/note= "opt glucosamine. 22</pre>	may "	have	mannose,	fucose,	glucose	or N-Ac-
ied-site	"opt mine.	may "	have	mannose,	fucose,	Œ	or N-Ac-
ified-site	<pre>/note= "opt glucosamine. 28</pre>	may "	have	mannose,	tucose,	Ф	or N-Ac-
. !	"opt mine.	may "	have	mannose,	fucose,	glucose	or N-Ac-
	"opt mine.	may	have	mannose,	fucose,	glucose	or N-Ac-
ied-sit	/note= "opt glucosamine.	may	have	mannose,	fucose,	glucose	or N-Ac-
ied-sit	"opt	may.	have	mannose,	fucose,	Ø	or N-Ac-
ified-site	"opt umine.	may "	have	mannose,	fucose,	glucose	or N-Ac-
ied-sit	"opt mine.	may	have	mannose,	fucose,	glucose	or N-Ac-
	"opt amine.	тау Мау	have also	mannose, have non	fucose inter	, glucose fering sub	se or N-Ac- substits."
219248-A1.							
NOV-1992.							

91US-00694983 92WO-US003609.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This compound represents a glycopeptide effective in inhibiting the binding of labelled mannosylated BSA to mannose receptors. Mannose receptors are uniquely found on macrophages and not on monocytes. Glycopeptides such as this provide a mechanism to target macrophages specifically, to image, label, destroy or otherwise alter their antigen grocessing function. In addition they can be conjugated to solid supports and used to purify mannose receptors from a variety of sources. They are useful in the treatment of inflammatory diseases driven by macrophage secretory products eg. Crohn's disease; infectious diseases in which macrophages harbour replicating infectious agents eg. Legionnaires disease, viral infections involving monnuclear phagocytes eg. HIV and lysosomal storage diseases; anthma mediated by alveolar macrophages; and in controlling metastasis, mediated by systemic macrophages. The peptides can also be used to deliver antigenic peptides as conjugates to a marchal an immune response; also self peptides to prevent tissue transplant rejection. (Updated on 25-MAR-2003 to correct PN
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                              Wang
Wall
                                                                                                       21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
WPI; 2003-029926/02
                                                                                                                                                                                                                                                                   WO200277183-A2
                                                                                                                                                                                                                                                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                                                                                                                                                                                                              Protein encoded by Prokaryotic essential gene #14086
                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU28559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU28559 standard; protein; 421 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 46 AA;
                                                                                                                                                                                                       21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                         03-OCT-2002
                                                                                                                                                                                                                                                                                                   Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New high affinity mannose receptor ligand cpds. - for treating diseases mediated by macrophage activity e.g. asthma, inflammatory diseases and infectious diseases, e.g. HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-398516/48
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                                                                             ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                            Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.0%;
                                           Malone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 98; DB 2;
Pred. No. 0.00082;
1; Mismatches 1;
                                         Haselbeck R,
                              Yamamoto R,
                            Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Indels
                          Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 46;
                            Zyskind Xu HH;
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Query Match Best Local

Similarity

46.0%;

Length 421;

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the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational and the carried of the c
Sequence 421 AA;
                                                                                                                           drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ACA32429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25; SEQ ID NO 56483; 1766pp; English.
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RX BX RX SX RX BX AX X
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                                                                                                                                                                                                                                                                                                                                           Matches
21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
                                   21-MAR-2002; 2002WO-US009107.
                                                                                                        Klebsiella pneumoniae
                                                                                    WO200277183-A2
                                                                                                                                  Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                         Protein encoded by Prokaryotic essential gene #16924.
                                                                                                                                                                                 19-JUN-2003 (first entry)
                                                                                                                                                                                                                                ABU31397 standard; protein; 323 AA
                                                                                                                                                                                                                                                                                            247 KKAAEKAAAEKAAADKKAAAEKAAADKKAAA-AKAAAEKAAAAKAAAEA 294
                                                                                                                                                                                                                                                                                                                                          32;
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                           <u>ب</u>
                                                                                                                                                                                                                                                                                                                                          Score 98; DB 6;
Pred. No. 0.008;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC encoding a polypoptide whose expression is inhibited by the antisense conucleic acid; (2) a host cell containing the vector; (3) an isolated conucleic acid; (2) a host cell containing the vector; (3) an isolated copolypoptide or its fragment whose expression is inhibited by the cantisense nucleic acid; (4) an antibody capable of specifically binding the polypoptide; (5) producing the polypoptide; (6) inhibiting cellular conclideration; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway capable of specifically binding cellular proliferation; (7) identifying a compound that influences the activity of identifying a gene required for cellular proliferation or the biological pathway capathway in which a proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound is activity; (11) a culture comprising strains in which the gene compound search of the strains is present in a culture or collection of the proliferation of an organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational contributed for proliferation in cells other than S. aureus S. typhimurium, capatived for proliferation in cells other than S. aureus S. typhimurium, capatived for part of the printed specification, but was obtained contribution. Format directly from WIPO at the sequence data for this capathypolitic sessential penes. Note: The sequence data for this capathypolitic sessential penes. Note: The sequence data for this capathypolitic sessential penes. Note: The sequence data for this capathypolitic sessential penes. Note: The sequence data for this capathypolitic sessential penes. Note: The sequence data for this capathypolitic sessential penes. Note: The sequence data for this capathypolitic sessential penes.
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 27
                                                             Listeria monocytogenes protein #1827.
  Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                                                                         05-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-2001; 2001US-0342923F
08-FEB-2002; 2002US-00072851
06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                           ABB49123 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
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                                                                                                                                                                                                                                                                                                                                        l Similarity
27; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELITRA PHARM INC.
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                                                                                                                                                                                                                                                                                                 Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 59321; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                      (first entry)
                                                                                                                                                                                           protein; 239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        44.6%;
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                    Score 95; DB
Pred. No. 0.01
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 323; 0.013;
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Forsyth
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                    6,
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infection; disease

Listeria monocytogenes

Antisense; prokaryotic essential gene; cell proliferation; drug design

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                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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Dussurget O, Chetouan...

Daniels J, Goebel W, Kreft J, Kuhn M, Syr-Z-Mar

Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Mar

Chakraborty T, Domann E, Hain T, Berche P, Chal

Perez-Diaz J, Baquero F, Garcia Del Portillo F,

Maduenio E, De Pablos B, Wehland J, Kaerst U,
                                                                Protein encoded by Prokaryotic essential gene #18146
                                                                                                       19-JUN-2003
                                                                                                                                         ABU32619;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic sequence for Listeria monocytogenes, useful e.g.\ for\ treatment and prevention of Listeria and related bacterial infections, and related
                                                                                                                                                                         ABU32619 standard; protein; 239
                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; SEQ ID NO 1828; 192pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-010914/01.
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                                                                                                                                                                                                                                                                124 KAAAEKAEADKKKQEEDAVKAANAKKEQEAAEEKAAADKAAAEKAAAE 171
                                                                                                                                                                                                                                                                                                  l Similarity
27; Conserv
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                   (first entry)
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Chetouani F,
                                                                                                                                                                                                                                                                                                                                                     56.2%;
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                                                                                                                                                                                                                                                                                                                                                     Score 94.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                      .011;
                                                                                                                                                                                                                                                                                                                                                                     DB 5; Length 239;
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                                                                                                                                                                                                          CC the 6213 antiteense sequences given in the specification where expression co of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid comprising a promoter operably linked to the nucleic acid composition where expression is inhibited by the antisense mucleic acid; (2) a host cell containing the vector; (3) an isolated complete containing the vector; (3) an isolated composition of the fragment whose expression is inhibited by the antisense composition of the containing the vector; (3) an isolated composition of the containing the polypeptide; (6) inhibited by the activity of a gene in an operon required for proliferation, or that influences the activity of groundifferation or the activity against a biological pathway of the gene product or that has an activity against a biological pathway or in which a proliferation or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an organism acts is present in a culture or collection of the strains is present in a culture or collection of compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for cidentifying proteins or screening for homologous nucleic acids required cory programs, or for screening homologous nucleic acids required cory programs, or for screening homologous nucleic acids required cory programs, or for screening homologous nucleic acids required cory programs, or for screening homologous nucleic acids or the target prokaryotic essential genes. Note: The sequence data for this cory programs differently from WIPO at
                                                                             Matches
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                                                                                         Sequence 239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25; SEQ ID NO 60543; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2002; 2002WO-US009107.
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                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ELIT-) ELITRA PHARM INC.
124
                                                                           l Similarity 56.:
27; Conservative
                                  KAAAEKAEADKKKOEEDAVKAANAKKEOEAAEEKAAADKAAAEKAAAE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zamudio C,
Trawick JD,
                                                                                            44.48;
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                                                                           7;
                                                                         Score 94.5; DB Pred. No. 0.011; Mismatches
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                                                                                                                DB 6; Length 239;
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Forsyth RA,
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                                                                             Indels
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Xu HH;
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                                                                           2;
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RESULT 15
AAR06445
ID AAR06

AAR06445 standard; protein; 154 AA

Search completed: April 20, 2004, 23:15:46 Job time: 31.2208 secs

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                                                                                                                                                                   To improve the expression of rCOP-1 polypeptides in E. coli, genes coding CC for rCOP-1-77 were subcloned from pREV 2.1 to pBG3-deltaN (deposit: 20-CC NOV-1984 US4691009, NREL B-15910); a plasmid used to express Protein A. CC The resulting plasmids encode fusion proteins consisting of beta cocurs between the Protein A, and rCOP-1 sequences. A methionine residue CC occurs between the Protein A and rCOP-1 sequences, originating from the CC incher sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1-77 contains ollypeptide may be cleaved CC incoding the following segments: YKK, EAE, KAK, AAK, and AAA. The N-CC terminal alanine residue is left behind following CNBT cleavage of the CC encephalomyelitis. They are used to prevent, arrest or control a CC demyelihating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged CC also ADDREGE (Inchert of context deficient in certain amino acids. See also ADDREGE (Inchert of context deficient in certain amino acids. See
                                                                                 Matches
                                                                                                                       Query Match
                                                                                                                                                                 Sequence 154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or immunological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1990-255848/34.
N-PSDB; AAQ05664.
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07-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant copolymer 1; COP-1-77; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis; multiple sclerosis.
                                                                                                                                                                                                        also AAQ05665. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 11; 25pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant copolymer 1-77, myelin basic protein analogue.
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03-JAN-1991
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                                                                                                   Match 44.1%;
Local Similarity 60.5%;
105
                                                                               26;
                                         2 KKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYE 44
  KKYKKKAKKAKYKK--KAKEAEKA----KAAAEAEKAKEAEYK 141
                                                                               Conservative
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(first entry)
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                                                                                 Mismatches
                                                                                                   Score 94; DB 2; Length 154; Pred. No. 0.0077;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein - protein search, using sw model
Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

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11: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

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213
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

15	14	13	12	11	10	φ		7						Д.	Result No.
89.5	Д	91	91	94.5	95	98	108	108.5	120.5	126.5	131	134.5	138	213	Score
42.0	42.0	42.7	42.7	44.4	44.6	46.0	50.7	50.9	56.6	59.4	61.5	63.1	64.8	100.0	Query Match 1
214	214	223	223	239	323	421	ω 5	428	66	86	77	56	109	45	Length
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US-10-282-122A-64817	TIS-10-282-1224-62547	US-10-205-979-52	US-10-051-643-201	US-10-282-122A-60543	US-10-282-122A-59321	US-10-282-122A-56483	US-09-816-989A-1	US-10-282-122A-55748	US-09-816-989A-4	US-09-816-989A-6	US-09-816-989A-5	US-09-816-989A-3	US-09-816-989A-7	US-09-816-989A-2	ID
Sequence 64817,	ייי ייי	e 52, 1	Sequence 201, App	60543,	Sequence 59321, A	5	Sequence 1, Appli	Sequence 55748,	.4	<u>ب</u>	ű	Sequence 3, Appli	,1	Sequence 2, Appli	Description

RESULT 2 US-09-816-989A-7

Sequence 7, Application US/09816989A

	44	43	42	41	40	39	38	37	36	35	34	<b>ω</b>	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
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Sequence 559, App	5.70	Sequence 292, App	<ol> <li>Appli</li> </ol>	e 419, Ap	e 259	e 7819	e 602	e 32,	æ	e 40,	392,	e 38,	e 39,	e 757	e 10923,	Sequence 24, Appl	e 12370,	nce 5398	'n	e 61735,	e 7504	ce 37076,	υı	e 67145,	Ψ.	e 120, Ap	e 6623	e 68109,	Sequence 27, Appl

### ALIGNMENTS

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                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-2
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US-09-816-989A-2
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09816989A Patent No. US20020115103A1 GENERAL INFORMATION:
                                                                                       Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 45; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MAI TITLE OF INVENTION: AND FOR THERAPEUTIC USE FILE REFERENCE: 2609/60807-A-PCT-US CURRENT APPLICATION NUMBER: US/09/816,989A CURRENT FILING DATE: 2001-03-23 PRIOR APPLICATION NUMBER: 60/101,693 PRIOR APPLICATION NUMBER: 60/101,693 PRIOR APPLICATION NUMBER: 60/101,693 PRIOR FILING DATE: 1998-09-28 PRIOR FILING DATE: 1998-09-28 PRIOR FILING DATE: 1999-09-24
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                                                                                                                                                                                                                                                     LENGTH: 45
TYPE: PRT
ORGANISM: Artificial Sequence
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                         1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
  AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
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                                                                                                              Score 213; DB 9;
Pred. No. 1.9e-16;
                                                                                            Mismatches
                                                                                                                                       Length 45;
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US-09-816-989A-5
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; Sequence 5, Application US/09816989A Patent No. US20020115103A1 ; GBUERAL INFORMATION: APPLICANT: Gad, Alexander
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LENGTH: 56
TYPE: PRT
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TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
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APPLICANT: Lis, Doris
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                                                                                                                                                                                                                                  1 АККҮАКК-----АКАЕКА-----ККАҮКАЛЕАКК--ААКҮЕКАЛАЕКАЛАКЕЛАҮЕА 45
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                                                                                                                                                                                                                                                                                                        63.1%;
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Pred. No. 7.9e-08;
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SEQ ID NO 6
LENGTH: 86
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Best Local S
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TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARF
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILLING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-24
NUMBER: OF SEQ ID NOS: 7
COMMENCE OF SEQ ID NOS: 7
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PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
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61 YKAEAAKKAYKAEAAKAAKEAAYEA 86
                                         30 -----KAAAEKAAAKEAAYEA 45
                                                                                                                                                                         39;
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                                                                                                                                                                      Conservative
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45.3%;
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                                                                                                                                                                    Score 126.5; DB 9; Pred. No. 9.3e-07; 0; Mismatches 6;
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Pred. No. 2.7e-07;
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RESULT 6

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                                                                                                               PRIOR FILING DATE: 2000-09-
PRIOR APPLICATION NUMBER: 6
PRIOR FILING DATE: 2000-10-
PRIOR APPLICATION NUMBER: 6
PRIOR FILING DATE: 2000-11-
PRIOR APPLICATION NUMBER: 6
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TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
NUMBER OF SEQ ID NOS: 7
SOFTMARE: Patentin version 3.1
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
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                          APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
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Zamudio, ca
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LENGTH: 428
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PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
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TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MA
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
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SOFTWARE: Patentin version 3.1
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                                                                                          APPLICANT
:ITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
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Zyskind, Jud
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Malone, Cheryl
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                                                                                                                    Yamamoto, Robert
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Pred. No. 3.6e-05
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 56483
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Best Local Similarity
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                                                                                                                                        APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
                                                                          PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
ADDITION NUMBER: 60/257,931
APPLICATION NUMBER: 60/242,578
                                     APPLICATION NUMBER: 60/230,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2001-02-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/267,636 FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
                      FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
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Malone, Cheryl
Haselbeck, Robert
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                        2000-09-
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; ORGANISM: Klebsiella pneumoniae US-10-282-122A-59321
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PRIOR FILLING DATE: 2000-11-27
PRIOR PELICATION NUMBER: 60/257,931
PRIOR FILLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILLING DATE: 2001-02-16
PRIOR FILLING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 60543
LENGTH: 239
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 59321
LENGTH: 323
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Publication No. US20040029129A1
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
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PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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27; Conserv
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Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
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lio, Carlos
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Pred. No.
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APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
APPLICANT: Tan, Paul L. J.
APPLICANT: Tan, Paul L. J.
APPLICANT: Abernethy, Nevin
TITLE OF INVENTION: Compounds and Methods for the Modulation
ITITLE OF INVENTION: of Immune Responses
FILE REFERENCE; 1100.1063U
CURRENT APPLICATION NUMBER: US/10/205,979
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/308,446
PRIOR APPLICATION NUMBER: 60/308,446
PRIOR FILING DATE: 2001-07-26
INUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 52
LENGTH: 223
                                                                                                 ; TYPE: PRT ; ORGANISM: Mycobacterium vaccae US-10-205-979-52
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US-10-205-979-52
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Query Match
Best Local Similarity
Matches 28; Conserv
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CURRENT FILLING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US09/156,181
PRIOR FILING DATE: 1998-09-17
PRIOR PELICATION NUMBER: US 08/996,624
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
TITLE OF INVENTION: System using Mycobacterium Vaccae
FILE REFERENCE: 11000.1008c2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 42.7%;
Local Similarity 59.6%;
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1 Similarity 56.2%;
27; Conservative
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         Conservative
                          42.7%;
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                          Score 91; DB 14; Length 223; Pred. No. 0.019;
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       Mismatches
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US-10-282-122A-64817

Sequence 64817, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:

APPLICANT: Wang, Liangsu APPLICANT: Zamudio, Carlo APPLICANT: Malone, Cheryl RESULT 15

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PRIOR FILING DATE: 2000-09-06
PRIOR PEPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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APPLICANT: Wang, Li
                                                                                            Matches
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APPLICANT:
APPLICANT:
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                                                                                                                                          Query Match
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2000-12-2
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23 PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                   Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
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                                                                                                                                                                                                               ORGANISM: Mycobacterium bovis
                                                                                                                                                                                                                                                                ENGTH: 214
                                                                                                                   Local
111 AKKVAKKAPAKKATKAAKKAATKAPA---RKAATKAPAKKAATKA 152
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                            1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
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                                                                                                                Similarity
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Zyskind, Jud
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Malone, Cheryl
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                                                                                            Conservative
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                                                                                  42.0%; Score 89.5; DB 12; Length 214; 55.6%; Pred. No. 0.026; Vative 4; Mismatches 13; Indels 3
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2000-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
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PRIOR PRIOR PRIOR DATE: 2000-10-23
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PRIOR PRIOR DATE: 2000-10-23
PRIOR BULLING DATE: 2000-10-23
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PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: Patentin version 3.1

SEQ ID NO 64817

IENGTH: 214

TYPE: PRT
ORGANISM: Mycobacterium tuberculosis

US-10-282-122A-64817
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Search completed: April 20, 2004, 23:27:17 Job time: 23.2078 secs
                                                                                                                                                                                                                                   Query Match 42.0%; Score 89.5; DB 12; Length 214; Best Local Similarity 55.6%; Pred. No. 0.026; Matches 25; Conservative 4; Mismatches 13; Indels 3.
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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Yamamoto, Robert
Forsyth, R.
Xu, H.
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Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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181.
181.5
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163.5
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1: pir1:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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pir3:*
pir4:*
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S61926
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S51364
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TolA colicin impor
mst101-1 protein -
histone H1-beta, e
sperm tall-specifi
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histone H1 - Chlam
                                                                                                                             outer membrane
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TolA protein PA097
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regulatory protein	2 A35630		340	28.3	147	45	
hypothetical prote	AE1689		243	28.3	147	44	
histone H1 - mouse	8 849482		221	28.3	147	43	
histone Hl.1 - Cae		N	208	28.3	147	42	
histone H1 - mouse			219	28.4	147.5	41	
histone H1 - musco	801262		218	28.5	148	40	
histone H1 (clone	106257		288	28.9	150	39	
histone H1-gamma,	PA26721		217	28.9	150	38	
histone H1 - mouse			212	28.9	150	37	
probable translati	T11583		1403	29.1	151	36	
histone H1.03 - ch	2 D28456		224	29.4	152.5	35	
outer membrane int	2 G64064		372	29.6	153.5	34	
conserved hypothet	H71321		369	29.6	153.5	33	
polyhydroxyalkanoa	2 G83013		309	29.8	154.5	32	
histone H1-II - Vo	2 JN0748		241		154.5	31	
hypothetical prote	2 529309		217	29.8	154.5	30	

#### ALIGNMENTS

C;Species: Escherichia coli
C;Date: 07-Sep-1990 #sequence revision 07-Sep-1990 #text\_change 01-Mar-2002
C;Accession: JV0057; B64810
R;Levengood, S.K.; Webster, R.E.
J. Bacteriol. 171, 6600-6609, 1989
A;Title: Nucleotide sequences of the tolA and tolB genes and localization of their prova, Reference number: JV0057; MUID:90078104; PMID:2687247
A;Accession: JV0057; MUID:90078104; PMID:2687247
A;Accession: JV0057

tolA protein -

Escherichia coli (strain K-12)

A;Cross-references: GB:M28232; NID:g148018; PIDN:AAA24683.1; PID:g148019
A;Experimental source: strain JM105

A; Molecule type: DNA A; Residues: 1-421 <LEV>

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repetitive protein histone H1 - rainb histone H1-5 [vali histone H1.11R - c histone H1-4 [vali h-caldesmon - chic
                                                                                                                                                                                     cytosolic repetiti
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protein VC183
RESULT
F90725
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A;Start codon: GTG
G;Keywords: nucleotide binding; P-loop; transmembrane protein
F;14-34/Domain: transmembrane #status predicted <MSS>
F;78-301/Domain: helical #status predicted <HSR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AAC73833.1; PID:g178696(A;Experimental source: strain K-12, substrain MG1655
C;Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Note: the authors translated the initiation codon GTG for residue 1 as Val R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; (A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID: 97426617; PMID: 9278503
A;Accession: B64810
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                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                        AKKEAY-KAEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAKAAKEAA 106
                                                                                                                                                                                                              ABEAAKQAELKQKQAEEAAAKAAADAKAKAEADAKA--AEEAAKKAAADAKKKAEAEAAK 177
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                                                                                                                                                                                                                                                                                                                                          36.5%; Score 189.5; DB 2
53.0%; Pred. No. 1.6e-05;
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163.5 162.5 161.5 161.5 160.5 160.5

HSHU1B A33430 A23055

HSTR1R S51660 C28456 A44993 E60110 B28456 T30296 A82152

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RESULT 3
G85576
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A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
Nucleic Acids Res. 14, 8121-8133, 1986 A; Title: Comparison of the late H1 histone genes of the sea urchins Lytechinus
                                                          histone H1 - sea urchin (Lytechinus pictus)
G;Species: Lytechinus pictus (painted urchin)
G;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-Jul-1999
G;Accession: A25550
R;Knowles, J.A.; Childs, G.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Nov-2001 C;Accession: G85576 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli
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                                                                                                                                                                                                                                                RESULT 4
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A; Residues: 1-394 <STO>
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
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A; Residues: 1-394 <HAY>
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R;Hayashi, T.; Makir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 AEEAAKQAELKQKQAEEAAAKAAAADAKAKAEADDKA--AEEAAKKAAADAKKKAEAEAAK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 AKKEAY-KAEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKAE----KAYAKKAKAAKEKKAYAKKEAKAYKAABAKKKAKAEAKKYAK-EAAK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 АККУАККАБ----КАУАККАКААКЕККАУАККЕАКАУКАБАКККАКАЕАККУАК-ЕААК 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                        AKKEAY-KAEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                AEEAAKQAELKQKQAEEAAAKAAADAKAKAEADDKA--AEEAAKKAAADAKKKAEAEAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.0%;
52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.0%; Score 181.5; DB 2; 52.2%; Pred. No. 4.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 181.5; DB 2; Length 394; ; Pred. No. 4.7e-05; 12; Mismatches 32; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                              232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D.J.; Mayhew K.; Apodaca,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>υ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       substrain
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      pictus
         an
                                                                                                                                                                                                                                                                                                                    tolA protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CTIE C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AG0592
   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <PAR>
                                                                                                            , S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Teference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             닭
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                                                                                                                                                                                                                                                             R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
                                                                                      A; Accession: AG0592
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:X04488; NID:g9616; PIDN:CAA28177.1; PID:g9617 C;Superfamily: histone H1 C;Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: strain PAO1 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: E83525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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A; Residues: 1-210 < KNO>
RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG04360.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TolA protein PA0971 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A25550; MUID:87040778; PMID:3022245
A;Accession: A25550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-347 <STO>
                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
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                                                                                      159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 КРАККААККРААК--КААККРААККРАККААККРААККААКРАККААККРААККАА 208
                                                                                                                                           60 AYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                      54
                                                                                                                                                                                                                                                           6 ККАЕКАҮАККАКААКЕК-----КАҮАККЕАКАҮКААЕАКККАКАЕАККҮАКЕААКҚЕ 59
                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E83525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                      A-EDEAKK--KAAEDAKKK-AAEDAKKKAAEEAKKKAAAEAAKKKAAVEA
                                                                                                                                                                                                      QKLEQQQVAAAKAAEQKKADEARKAEAQKAAEAKKADEAKKAAEAKAAEQKKQADIAKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEAYKAEAKKYAKAAKAEKKEYAAAEAKKA-----EAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTEAQKA-RAAAKKAKLAAKKKEQKEKKAAKTKARKEKLAAKKAAKKVAKKVAKAK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAE----AKKKAKAEAKKYAKEAAKAK 57
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                              34.5%;
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                                                                                                                                                                                                                                                                                                                      17; Mismatches
                                                                                                                                                                                                                                                                                             Score 179; DB 2;
Pred. No. 6.2e-05;
Pred. No. 6.2e-05; Indels
                                                                                                                                                                                                                                                                                                                                                                             Length 347;
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K.; Lim,
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Skelton, J.; Stevens Salmonella enterica

Stevens,

serov 7

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RESULT 8
S34153
A,Gene: FlyBase:Dhyd/mst101
A;Cross-references: FlyBase:FBgn0011816
C;Superfamily: neurofilament triplet H protein
                                                                             A;Cross-references: EMBL:X73480; NID:g313199; PID:g313200 C;Genetics:
                                                                                                                         A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-344 <NEE>
                                                                                                                                                                                                                                             C;Accession: S34153
R;Neesen, J.; Heinlein, U.A.O.; Buenemann, H. submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                   mst101-1 protein - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AC0138
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A;Gene: STY0793
                                                                                                                                                                                               A; Reference number: S34153
A; Accession: S34153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-388 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarragg, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, I.M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre Nature 413, 523-527, 2001
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                                                                        ;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 KQAAEQQKIAAAAVAKAEEQKQAETAAAQAKAEADKIVKAQAEAQKKAEAEAKKEAAVA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 AKAAADAKKKAEAEAAKAAADAKKKAEAEA-AKAAADAKKKAEAEA---AKAAAEAKK-- 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 -KAEAEAAKAAADAKKKADAEAAKAAAEAKKKADAAAAKAAADAKKKAAAE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 AKAKKEAYKAEAKKYAKAAK-----AEKKEYAAAEAKKAEAAK--AYKAEAAKAAAKEA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAA---KEAAYE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 АККУАККАЕКАУАККАКААКЕККАУАККЕАКАУКААЕАКККАКАЕАККУАКЕААКАККЕА 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 178; DB 2; Length 388 Pred. No. 7.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 178; DB 2; Length 376 Pred. No. 7.6e-05;
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A;Molecule type: DNA
A;Residues: 1-163,'E',164-236,'Q',237-254,257-320,'E',321-1390 <NEW>
A;Cross-references: EMBL:X73481; NID:g313201; PID:g313202
                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-1390 <RES>
A;Cross-references: EMBL:X73481
A;Cross-references: EMBL:X73481
R;Neesen, J.; Heinlein, U.A.O.; Buenemann, H.
submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif repre: lpha-helical rods within the extremely elongated spermatozoa of Drosophila hydei. A;Reference number: S51364; MUID:95045538; PMID:7957199
A;Accession: S51364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K;Neesen, J.; Padmanabhan, S.; Buenemann, H. Eur. J. Biochem. 225, 1089-1095, 1994
A;Title: Tandemlv arrance
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C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; embryo; nucleosome; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Lai, Z.C.; Childs, G.

Mol. Cell. Biol. 8, 1842-1844, 1988
A; Title: Characterization of the structure
A; Reference number: A28100; MUID:88246461;
A; Accession: A28100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        histone H1-beta, embryonic - sea urchin (Strongylocentrotus purpuratus) c;Species: Strongylocentrotus purpuratus (purple urchin) C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 23-Feb-1997 C;Accession: A28100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
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A; Accession: S34154
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                                                                                            A; Cross-references: FlyBase: FBgn0011816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                       A;Gene: mst101(2)
                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: nucleic acid sequence not shown
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Best Local
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Best Local :
                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 --АККЕАҮКАЕАККҮАКААККЕККЕҮАААЕАККАЕААКАҮКАЕААКАААКЕАА 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 KLGKKKEGKSDAQKARDAAKKAKLAAKKKEAKEAKEKKAARSKAKKEKLAAKKASKKTTKKVK 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55
57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKKAEK----AYAKKAKAAKEKKAYAKKEAKAYKAAE-----AKKKAKAEAKKY 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPAAKKAKKPAAKKAAKKPAAKKPAAKKAAAKPAPAKKAAKKPAAKKAAKKVA 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKK 124
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.2%;
48.7%;
                      33.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 175.5; DB Pred. No. 0.0001; B; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
Score 171.5; DB (
Pred. No. 0.00051)
1; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 172.5; DB 2; Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and transcriptional patterns of the gene enepMID:2837660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                               DB 2;
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                                               Length 1390;
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  15;
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  Gaps
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histone H1, gonadal - sea urchin (Parechinus angulosus)
C;Species: Parechinus angulosus (angulate urchin)
C;Date: 31-Mar-1980 #sequence_revision 31-Mar-1980 #text_change 16-Feb-1997
C;Accession: A91090; A91091; A02586
C;Accession: A91090; A91091; A02586
Eur. J:Biochem. 104, Strickland, M.; de Groot, P.C.; von Holt, C.; Wittmann-Liebold, B.
Eur. J. Biochem. 104, 559-566, 1980
A;Title: The primary structure of histone H1 from sperm of the sea urchin Parechinus anguminal cyanogen bromide peptides.
A;Reference number: A91090; MID:80156831; PMID:6767609
A;Contents: sequence of residues 1-84
A;Accession: A91090
                                                                                                                                                                                                                                                                                                                                                                        C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999 (;Accession: T09127  
C;Accession: T09127  
R;Kappe, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H. Proc. Natl. Acad. Sci. U.S.A. 95, 1230-1235, 1998  
A;Title: A family of chimeric erythrocyte binding proteins of malaria parasites. A;Reference number: Z16577; MUID:98115903; PMID:9448314  
A;Accession: T09127
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C;Superfamily: histone H1
C;Keywords: DNA binding; nucleosome; sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 1-248 <STr.
R; Strickland, W.N.; Strickland, M.; Brandt, W.F.; von Holt, C.; Lehmann, A.; Wittmann-Li
Eur. J. Biochem. 104, 567-578, 1980
A; Title: The primary structure of histone H1 from sperm of the sea urchin Parechinus ang
A; Reference number: A91091; MUID:80156832; PMID:7363905
                                                                                          A;Introns: 62/1; 1040/1; 2077/2; 2077/2
C;Keywords: alternative splicing; cell binding; erythrocyte invasion
                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-1701 <KAP>
A; Cross-references: EMBL: AF031886; NTD: 92947227; PID: 92947228
A; Experimental source: subspecies yoelii; strain YM
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T09127
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                                                                                                                                                                                 A;Gene: maebl
      Matches
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                                                                                                                                                   Introns: 62/1; 1648/1; 1674/2; 1697/1
                                       Local
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      54;
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                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KA--EAKKYAK-----AAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKAKKTSAAAKAKKAKAAAAKKARKAKAAAKRKAALAKKKAAAAKRKAAAKAKKAKKPKK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKEAAKAKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
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         Conservative
32.9%; Score 170.5; DB 2
53.5%; Pred. No. 0.00068;
tive 11; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.9%; Score 170.5; DB 1; 46.0%; Pred. No. 0.00017;
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                                                      DB 2; Length 1701;
         31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 248;
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      Matches
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histone H1 - Chlamydomonas reinhardtii
(;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 10-Apr-1996 #Bequence_revision 19-Apr-1996 #text_change 23-Jul-1999
C;Accession: S59589; 862122
R;Fabry, S.; Mueller, K.; Lindauer, A.; Park, P.B.; Cornelius, T.; Schmitt, R.
Curr. Genet. 28, 33-345, 1995
A;Title: The organization structure and regulatory elements of Chlamydomonas histone ger
A;Reference number: S59581; MUID:96120862; PMID:8590479
                                                                                                                                     A;Introns: 62/3; 101/3
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U16726
A;Note: the authors did not translate the codon for residue 1
R;Fabry, S:, Ford, C., Lindauer, A.; Mueller, K.; Cornelius, T.; Schmitt, R.
submitted to the EMBL Data Library, October 1994
A;Description: The organization, structure and controlling elements of Chlamydomonas his
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C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 04-Mar-2000
C;Accession: A28456
R;Coles, L.S.; Robins, A.J.; Madley, L.K.; Wells, J.R.E.
J. Biol. Chem. 262, 9656-9663, 1987
A;Title: Characterization of the chicken histone H1 gene complement. Generation of a cor A;Reference number: A92655; MUID:87250632; PMID:3597432
                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-173,'P',174-231 <FAW>
A;Cross-references: EMBL:U16726; NID:g571479; PIDN:AAA98452.1; PID:g571480
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Description: The organization, A;Reference number: $62122
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                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S62122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S59589
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A; Residues: 1-220 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-231 < FAB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
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                                      31.7%; Score 164.5; DB 2; 45.9%; Pred. No. 0.00038;
       10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Mismatches
       39;
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Cgcr-4 protein - Chlamydomonas reinhardtii (fragment)
C;Species: Chlamydomonas reinhardtii
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C;Accession: S19113; S14466
R;Wakarchuk, W.w.; Mueller, F.W.; Beck, C.F.
Plant Mol. Biol. 18, 143-146, 1992
A;Title: Two GC-rich DNA elements of Chlamydomonas reinhardtii with complex arrangements A;Reference number: S19113; MUID:92119224; PMID:1731966
A;Accession: S19113
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-265 WAKA
A;Residues: 1-265 WAKA
A;Cross-references: EMBL:X17208; NID:918136; PIDN:CAA35080.1; PID:918137
C;Genetics:
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S19113
Search completed: April 20, 2004, 23:18:23 Job time : 19.1104 secs
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                                                                                                             199 EAKAKEA 205
                                                                                                                                                                 103 KEAAYEA 109
                                                                                                                                                                                                                       139 КУАЛЕАКАЛАЛАЕЛКАЛАЛАЕЛАЛАКАКУАЛЕДКАЛАЛАЕЛАЛАЛАЕЛАЛАКАКАЛАЛ 198
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                                                                                                                                                                                                                                                                           47 KKYAKEAAKAKKEAYKAEAKKYAKAAK----AEKKEYAAAEAKKAEAAKAYKAEAAKAAA 102
                                                                                                                                                                                                                                                                                                                            79 AEAKAKEADEARAAEAEARAVAEAWAAAEAEARAEAEAWAAAEAEAWAAAEVEARAAAQA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 KAKKEAYKAEAKKYAKAA----KAEKKEYAAAE---AKKAEAAK---AYKAEAAKAAAKE 104
                                                                                                                                                                                                                                                                                                                                                                                   1 AKKYAKKAEKA-----YAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEA 46
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Result
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Maximum Match 100%
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
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519
1 AKKYAKKAEKAYAKKAKAAK......AKAYKAEAAKAAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     April 20, 2004, 23:08:59 ; Search time 14.8636 Seconds (without alignments) 381.848 Million cell updates/sec
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          SwissProt_42:*
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        HILE STRPU
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H1 LYTPI
TOLA PSEAE
MST1_DROHY
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H1 PARAN
H1B_STRPU
RL22_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                            P19934 escherichia
P06144 lytechinus
P50600 pseudomonas
Q08695 drosophila
Q08696 drosophila
P02256 parechinus
                                                                                                                  Q8eh15
Q08865
P44678
P08285
Q10475
P15864
P07796
                                                     Q93mh5
P09426
P43274
P10771
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P12957
P08284
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Q9zhc5
P08288
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O01395
Q9vgx3
P08286
                                                                                                                                                                                                                                                                                                                              P29720 treponema p
P08287 gallus gall
P06350 oncorhynchu
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                                                                                                                                                 5 mycobacteri
8 gallus gali
2 homo sapien
7 gallus gali
4 gallus gali
5 shewanella
5 volvox cart
8 haemophilus
5 gallus gali
5 schizosacch
 7 mus musculu
7 gallus gall
7 drosophila
                                                   6 anas platyr
4 mus musculu
1 caenorhabdi
                                                                                                     4 mus musculu
6 strongyloce
5 klebsiella
                                                                                                                                                                                                                                                                                                                                                                                gallus gall
                                                                                                                                                                                                                                                                                                                                                                                                 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                drosophila
                                                                                                                                                                                                                                                                                                                  homo sapien
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45	44	43	42	41	40	39	38	37	36	35	34
139	140	141.5	141.5	142	142.5	143	143	143	143.5	144	144
26.8	27.0	27.3	27.3	27.4	27.5	27.6	27.6	27.6	27.6	27.7	27.7
213	232	346	232	194	221	236	214	214	218	352	232
H	₩	μ	μ	₽-3	Н	Н	μ	ш	<b>}-4</b>	1-1	_
H13_RABIT	HIA CHITE	RS6 AEDAE	HIB CHITE	H1 SALTR	HIC CHITE	H1_NEUCR	DBH MYCTU	DBH MYCBO	H12 RAT	ALGP PSEAE	H12_GLYBA
P02251	P40275	Q9u761	P40276	P02254	P40277	Q8j0u2	P95109	81dx60	P15865	P15276	P40264
oryctolagus	chironomus	aedes aegyp	chironomus	salmo trutt	chironomus	neurospora	mycobacteri	mycobacteri	rattus norv	pseudomonas	glyptotendi

#### ALIGNMENTS

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tl. Acad. ION WITH 97133271; e R., Gav	AINS. LINE=91296736; engood S.K., E	ence of the Becherichia coli K he 12.7-28.0 min region on the 5(1996).	FROM N.A. 112; 97061202; Pu 97061202; Pu K., Inada H., K., Inada T. Kitagawa Motomura K.	SEQUENCE FROM N.A.  STRAIN=K12 / MG1655;  MEDLINE=97426617; PubMed=9278503;  MEDLINE=97426617; PubMed=778503;  Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  Mau B., Shao Y.;  "The complete genome sequence of Escherichia coli K-12.";  Science 277:1453-1474(1997).	SEQUENCE FROM N.A.  STRAIN-JM105;  MEDLINE-90078104; PubMed=2687247;  MEDLINE-90078104; PubMed=2687247;  Levengood S.K., Webster R.E.;  "Nucleotide sequences of the tolA and tolB genes and localization of their products, components of a multistep translocation system in Escherichia coli.";  J. Bacteriol, 171:6600-6609(1989).	TOLA OR CIM OR EXCC OR LKY OR B0739.  Escherichia coli.  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.  NCBI TaxID=562;  [1]	10-01 10-10 10-10 10-10 10-10 10-10 10-10 10-10

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RESULT 2
H1_LYTPI
ID H1_LYTPI
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Best Local
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STRAND
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-!- FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF GROUP A
                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                       TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transport; Protein transport; Bacteriocin transport; Transmembrane; Repeat; Inner membrane; 3D-structure; Complete proteome.
1 13 CTTOPLASMIC (POTENTIAL).
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Tracegene; EG11007; tolA.
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MEDLINE=99332679; PubMed=10404600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "TolA central domain interacts with Escherichia coli porins.", EMBO\ J.\ 15:6408-6415(1996).
                                                                                                                                                                                                                                                                                            TURN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; JV0057; JV0057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF GROUP A COLICINS (COLICINS A, E1, E2, E3, AND K). NECESSARY FOR THE COLICINS TO REACH THEIR RESPECTIVE TARGETS AFTER INITIAL BINDING TO THE BACTERIA. ALSO INVOLVED IN THE TRANSLOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: INTERACTS, VIA DOMAIN II, WITH PORINS OMPC, OMPC, PHOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF BACTERIOPHAGE DNA.
                                                                             178
                                                                                                                                          120
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ე
                                                                                                                                                                                                    61;
                                                                                                                                                                     Н
                                                                                                                                                                                                                   Similarity
                                                                            AAAEAQKKAEAAAAAKKKAEAAEAAAAEARKKAATEAAEKAKAEAEKKAAAEKA
                                                                                                         АККЕАУ-КАЕАККУАКААКАЕККЕУАААЕАКК---АБААКАУКАЕААКАААКЕАА 106
                                                                                                                                        AEEAAKQAELKQKQAEEAAAKAAADAKAKAEADAKA - AEEAAKKAAADAKKKAEAEAAK
                                                                                                                                                                     AKKYAKKAE----KAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKXAKAEAKKYAK-EAAK 55
                                                                                                                                                                                                                                                                421 AA;
                                                                                                                                                                                                    Conservative
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC73833.1; -.
                                                                                                                                                                                                                                                                                                                           358
369
372
383
397
                                                                                                                                                                                                                                                              43156 MW; 8B2F52B4B97C655E CRC64;
                                                                                                                                                                                                 36.5%; Score 189.5; DB 1
53.0%; Pred. No. 4.5e-06;
tive 11; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN II (ALPHA-HELICAL).

DOMAIN III (FUNCTIONAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 X TANDEM REPEATS OF [ED]-K(1,2)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PERIPLASMIC (POTENTIAL)
   PRT;
   210 AA
                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                    32;
                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                              421;
                                                                                                                                                                                                  11;
                                                                                                                                                                                                 Gaps
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RRROCCOGETTAC
                                                                                                                                                                                                                                 RESULT 3
TOLA_PSEAE
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                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 58
                                                                                                                                    P5560;
01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Late histone H1.
Lytechinus pictus (Painted sea urchin).
Eukaryota, Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea, Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                                                                                                  TOLA protein.
TOLA OR PA0971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0624; HISTONEH5.
ProDom; PD000373; Linkerhist_N; 1.
SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR005818; Histone_H1/H5
InterPro; IPR005819; Histone_H5
InterPro; IPR005316; Linkerinst N.
Pfam; PF00538; linker_histone; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X04488; CAA28177.1; -. PIR; A25550; A25550. HST. HSSP; P02259; 1HST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lytechinus pictus and Strongelocentrotus purpuratus.";
Nucleic Acids Res. 14:8121-8133(1986).
-!- FUNCTION: Histones H1 are necessary for the condensation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P06144;
01-JAN-1988
                                          NCBI_TaxID=287;
                                                            Bacteria, Proteobacteria, Gammaproteobacteria,
Pseudomonadaceae, Pseudomonas.
                                                                                                Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Knowles J.A., Childs G.J.; "Comparison of the sea
                SEQUENCE FROM N.A.
                                                                                                                                                                                                                    TOLA PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the histone H1/H5 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=87040778; PubMed=3022245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleosome chains into higher order structures. SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                     155 KPAKKAAKKPAAK--KAAKKPAAKKPAKKAAKKPAAKKAAKPAKKAAKKPAAKKAA
                                                                                                                                                                                                                                                                                                                                     58 KEAYKAEAKKYAKAAKAEKKEYAAAEAKKA-----EAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                       2 KKYAKKAEKAYAKKAAKEKKAYAKKEAKAYKAAE----AKKKAKAEAKKYAKEAAKAK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                         58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                       KTEAQKA-RAAAKKAKLAAKKKEQKEKKAAKTKARKEKLAAKKAAKKAAKKVKKPAAKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . protein; Nuclear protein; DNA-binding; Mul 210 AA; 21746 MW; 08C38F64894007E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.9%;
                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 181; DB 1;
Pred. No. 9.2e-06;
                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                    347 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
                                                                                Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     urchins
                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Gaps
                                                                                                                                                                                                                                                                                                                                                                       154
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STRAIN=PAO

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                                                                                                                          RESULT 4
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                             Query Match
Best Local
                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Axoneme-associated protein mst101(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufingle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentho E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Loson M.V., "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it the Ey non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ATCC 15692
MEDLINE=20437337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa.";
J. Bacteriol. 178:7059-7068(1996)
                                                                                                    MST1
                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR006260; TonB_C.
TIGRFAMs; TIGR01352; tonB_Cterm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neoptera; Endopterygota; Diptera;
         Drosophila hydei (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                MST101(1)
                                                                                         Q08695;
                                                                                                                DROHY
                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS TO N-TERMINUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97113525; PubMed=8955385;
                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: Involved in the tonB-independent uptake of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity)
                                                                                                                                                                                                                                                                                                                                                                                                      E83525; E83525.
                                                                                                  DROHY
                                                                                                                                                                                                                                                                                                                                                       ete proteome.
                                                                                                                                                            159
                                                                                                                                                                                                                                                                                                                                                                                                               AE004530; AAG04360.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                          U39558; AAC44660.2; -.
                                                                                                                                                                                 60
                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                    54
                                                                                                                                                                                                                              σ
                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                            A-EDEAKK--KAAEDAKKK-AAEDAKKKAAEEAKKKAAAEAAKKKAAVEA
                                                                                                                                                                                 АУКАЕАККУАКААКАЕККЕУАААЕАККАЕААКАУКАЕААКАААКЕААУЕА 109
                                                                                                                                                                                                                             KKAEKAYAKKAKAAKEK-----KAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKE
                                                                                                                                                                                                        QKLEQQQVAAAKAAEQKKADEARKAEAQKAAEAKKADEAKKAAEAKAAEQKKQADIAKKR
                                                                                                                                                                                                                                                                                           209
347
                                                                                                                                                                                                                                                                                                                                                                   Protein transport; Transmembrane; Repeat; Inner membrane;
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                 AA;
                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=10984043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / PAO1;
                                                                                                                                                                                                                                                                                                            347
216
                                                                                                                                                                                                                                                                                                 37935 MW;
                                                                                                                                                                                                                                                               34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the
                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                               Score 179;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                       PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sokol P.
                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                 EEDD4B04AA095945 CRC64;
                                                                                                                                                                                                                                                    Mismatches
Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the tolQRA
                                                                                                   344 AA
                                                                                                                                                                                                                                                               .9e-05;
                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                     29;
                                                                                                                                                                                                                                                                          Length 347;
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes of
                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a collaboration
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 밁
                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                        MST2_DR
Q08696;
                                                                                                                                                                                                                             DROHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995
01-FEB-1995
Neesen J., Padmanabhan S., Buenemann H.;
"Tandemly arranged repeats of a novel highly charged 16-amino-acid
motif representing the major component of the sperm-tail-specific
axoneme-associated protein family Dimstill form extended
alpha-helical rods within the extremely elongated spermatozoa of
                                                                                                                                                                                                                                                                                                                                                       Neoptera; Endopterygota; Diptera; Brack
Ephydroidea; Drosophilidae; Drosophila
NCBI_TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila hydei (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7224;
                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND CHARACTERIZATION MEDLINE=95045538; PubMed=7957199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MST101(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94200512; PubMed=8150205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The Drosophila hydei gene Dhmst101(1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Axoneme-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Base; FBgn0011816; Dhyd\mst101(1).
GO:0005737; C:cytoplasm; IDA.
GO:0005198; F:structural molecule activity; IEP.
GO:0007288; P:axoneme_assembly; IEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Possible structural role in the sperm tail. associated with axonemal structures. SUBCELULIAR LOCATION: Cytoplasmic (By similarity). TISSUE SPECIFICITY: Testis. Located in spermatocytes (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLYMORPHISM: The number of repeats varies between strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spermatid bundles.

DOMAIN: The predominant structure is alpha-helical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DROHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S34153; S34153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X73480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 АКБААКАККЕАУКАБАККУАКААКАЕККЕУАААБАКК-АБААКАУКАБААКАААКБАА 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 AKKEKEAAEKKKCAEAAKKEKEAABKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKAEK----AYAKKAKAAKEKKAYAKKEAKAYKAAE-----AKKKAKAEAKKY 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 40, Last annotation updat
ociated protein mstl01(2).
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19 X 16 AA APPROXIMATE TANDEM REPEATS
18 X 16 AA APPROXIMATE TANDEM REPEATS
19 X 16 AA APPROXIMATE TANDEM REPEATS
19 X 16 AA APPROXIMATE TANDEM REPEATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.8%;
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Pred. No. 3.
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P02256;
21-JUL-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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Eur. J. Biochem. 225:1089-1095(1994)
                                                                                                                                                                                                                                    "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 1. Chemical and enzymatic fragmentation of the protein and the sequence of amino acids in the four N-terminal
                         Strickland W.N., Strickland M., Wittmann-Liebold B.; "The primary structure of history
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parechinus angulosus (Angulate sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Histone H1,
  Parechinus angulosus. 2.
                                                                                                     MEDLINE=80156832;
                                                                                                                                    SEQUENCE OF 80-248.
                                                                                                                                                                                                        cyanogen
                                                                                                                                                                                                                                                                                                                 Strickland W.N., Strickland M., Wittmann-Liebold B.,
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=80156831; PubMed=6767609;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  VCBI_TaxID=7658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for content and the statement is not removed.
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DOMAIN: The
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SUBCELLULAR LOCATION: Cytoplasmic.
TISSUB SPECIFICITY: Testis. Primary spermatocytes and early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1128 CEEAAKREKEA--AEKKKCAEAAKKEKE--ATEKQKCAEAAKKEKEAAEKKKCAEAA 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S51364; S51364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 АКЕЛАКАККЕЛУКАЕЛККҮЛКАЛКАЕККЕУЛЛАЕЛККАЕЛАКАУКАЕЛАКАЛАКЕЛА 106
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                                                                                                                                                                                    . Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gonadal.
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                                                                                                                                                                                    peptides.";
104:559-566(1980)
                                                                                                        PubMed=7363905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.0%;
of histone H1 from sperm of the sea urchin
2. Sequence of the C-terminal CNBr peptide and
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Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                             de Groot P.C., von Holt C.,
                                                                            Brandt W.F., von Holt C., Lehmann A.,
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                                                                                                                                                                                                                                   "Characterization of the structure and transcriptional patterns of the gene encoding the late histone subtype H1-beta of the sea urchin Strongylocentrotus purpuratus.", Mol. Cell. Biol. 8:1842-1844 (1988).
-!- FUNCTION: Histones H1 are necessary for the condensation of nucleosome chains into higher order structures.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the histone H1/H5 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P15869;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Histone H1-beta, late embryonic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR005818; Histone_H1/H5.
InterPro; IPR005819; Histone_H5.
InterPro; IPR005316; Linkerhist_N.
Pfam; PF00538; linker_histone; 1.
PRINTS; PR00624; HISTONEH5.
                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -I- FUNCTION: Histones H1 are necessary nucleosome chains into higher order -I- SUBCELLULAR LOCATION: Nuclear.
EMBL; M20314; AAA30052.1; -.
PIR; A28100; A28100.
HSSP; P02259; 1HST.
InterPro; IPR005818; Histone_H1/H5.
InterPro; IPR005819; Histone_H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strongylocentrotus purpuratus (Purple sea urchin)
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00526; H15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the entire primary structure.";
Eur. J. Biochem. 104:567-578(1980).
                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=88246461; PubMed=2837660;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000373; Linkerhist_N; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: Sperm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 KKAKKTSAAAKAKKAKAAAAKKARKAKAAAKRKAALAKKKAAAAKRKAAAKAKKAKKPKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 KAAKKAKKPAKKSPKKAKKPAKKSPKKKKAKRSPKKAAKKAAGKRKPAAKKARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 KA--EAKKYAK-----AAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144
248 AA;
                                                                                                                                                                                                                                                                                                                                                                            Childs G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 I
26387 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K -> R.
; 1B25B3F136541947 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 170.5;
Pred. No. 5e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eleutherozoa; Echinozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 AA
                                                                                                                      noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        structures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for the condensation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                         EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                         a collaboration
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Best Local S
Matches 55
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               Query Match
Best Local
                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE=99372678; PubMed=10445506; Neesen J., Heinlein U.A.O., Heinz Glatzer K., Buenemann H.; Neesen With tandemly arranged repeats of a highly charged 16-amino-acid motif encoded by the Dhmst101 gene family are structural components of the outer sheath of the extremely elongated sperm tails
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DROHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                      of Drosophila hydei.";
Dev. Growth Differ. 41:93-99(1999).
                                                           SEQUENCE
                                                                                                                                                                                     EMBL; U85627; AAB51369.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00526; H15; 1.
                                                                                                                                                                        FlyBase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila hydei (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Axoneme-associated protein mst101(3).
MST101(3) OR DHMST101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0624; HISTONEH5.
ProDom; PD000373; Linkerhist_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003216; Linkerhist N. Pfam; PF00538; linker histone; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2003 (Rel.
10-OCT-2003 (Rel.
10-OCT-2003 (Rel.
                                                  TISSUE SPECIFICITY: Testis.
                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Possible structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 КРААККАККРААККААККРААККРААККАААКРАРАККААККРААККVA 200
54;
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                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --AKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KYAKKAE-KAYAKKA--KAAKEKKAYAKKEAKAYKAAEAK-KKAKAEAKKYAKEAAK--- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLGKKKEGKSDAQKAPDAAKKAKLAAKKKEAKEAKEAKSKAKKEKLAAKKASKKTTKKVK 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 AA;
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; Nuclear protein; DNA-binding; Multigene
211 AA; 22169 MW; 9F214581334BBE7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 42, Created)
(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
               32.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.7%;
48.7%;
 16;
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               Pred. No. 6.4e-05
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 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275 AA.
                                                                                                                                                                                                                                                                                                                                                                       in the sperm tail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.1e-05;
                         DB 1;
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                           Length 275;
 Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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RA Addms M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Amanatides P.G., Scherer S.E., Holt R.A., Hoskins R.A., Galle R.F., Ra Amanatides P.G., Scherer S.E., Holt R.A., Hoskins R.A., Galle R.F., Ra Berong R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N., RA Berondon R.C., Rogers Y.H.C., Blazej R.G., Champa Q., Chen L.X., Ra Ballew R.H., Doyle C., Baxeer E.G., Helt G., Nelson C.R., Miklos G.L.G., Ra Barlaw R.H., Dayle C., Baxeer B.G., Helt G., Nelson C.R., Miklos G.L.G., Ra Ballew R.M., Basu A., Baxendale J., Bayzaktaroglu L., Beasley E.M., Ra Ballew R.M., Basu A., Baxendale J., Bayzaktaroglu L., Beasley E.M., Ra Berson K.Y., Berman B.P., Bandari D., Bolshakov S., Ra Berson K.Y., Berman B.P., Brokstein P., Brottier P., Ra Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Certy J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Borkova D., Botchar A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Dorson K.J., Evangelista C.C., Ferriera S., Pleischmann W., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Ganan P., Harris M., Alaris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Jalain M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Alashin M., Harrish M.-H., Ibewam C., Alasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Liasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Liako P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Liako P., Lei Y., Levitsky A.A., Murph L., Mur
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAU DROM Q9VGX3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Canton-S; TISSUE=Head;
MEDLINE=99097004; PubMed=9878744;
Ma E., Xu T., Haddad G.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Pruit fly).
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster."
Brain Res. Mol. Brain Res
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Gene regulation by O2 deprivation: an anoxia-regulated novel gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 QEA--AQKKKCAELAKKEKE---AAEKKKCAEAAKKEKEAAERKKCEEAAFK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 KEAYKAEAKKYAKAAKAEKKEYAAAEAKK-AEAAKAYKAEAAKAAAKEAAYE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 AEDVKKKCEEAAAKKKCAEAAKKEKEAAEKK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q95818; Q9VGX1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brain Res. 63:217-224(1999).
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EMBL; AR154418; AAD38397.1; --
EMBL; AE003688; AAF54549.2; --
EMBL; AE003688; AAF54550.1; --
EMBL; AE003688; AAF54551.1; --
EMBL; AE003688; AAF54552.1; --
EMBL; AE003688; AAF54552.1; --
EMBL; AY0060997; AAL28545.1; --
EMBL; AY119569; AAM50223.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase: FLYBase; FLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: Plays an important role in the regulation
                                                                                         VARSPLIC
                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0020439; fau.
GO; GO:0006979; P:response
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SEQUENCE FROM N.A. (1501011)
STATE OF THE STATE OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Annotation of the Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDUCTION: By anoxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   responsiveness to oxygen deprivation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q9VGX3-5; Sequence=VSP 004052;
SSUE SPECIFICITY: Concentrated in la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q9VGX3-4; Sequence=VSP_004050,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9VGX3-3; Sequence=VSP_004046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q9VGX3-2; Sequence=VSP_004048,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q9VGX3-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isoforms;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol.
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                                                                                         163
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cortical neurons of central brain.
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                                                                                                                                                     ALA/GLU-RICH.

YPSVEKVTRVYKSSYPIYSSYSPRRYYGATRVYTSPIRVV
TSPARVYSRYLIPSYRVVRTITRVISSPERTTYSYTTPS
TYYSPSYLPSYTTSTYLPTSYTTY -> TPRLDLCTDRPGS
HRSRASSDYSYTSTKLPTSYTTY -> TPRLDLCTDRPGS
HRSRASSDYSYTSKSSVEKSSYDSSNPHSYRPERSTYTSTV
EKTSRSGPGGSYNYSTERTSTTGAGPGGYSYSSTTSGNLPG
GTKYRHFSYHV (in isoform C).

Missing (in isoform C).
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된
/FTId=VSP_004047.

/FTID=VSP_004047.

YBSVEKVTRVYKSSYPYYSSYSVPRRVYGATRVVTSPIRVV
TSPARVVSRVHSPSPRVVRUTTTRVISSERTTYSYTTPS
TYYSPSYLPSTYTSTYIPTSYTTYPSYAYSPTTVTRVYAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oxidative stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . Yu C., .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSP_004051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSP_004047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      euchromatic genome: a
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Prochnik S.E.,
L., Berman B.P.,
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Best Local S
Matches 55
                                                                                                                                                                                 MEDLINE=98060905; PubMed=9396815;
Schwarz S., Hess D., Jost J.P.;
"The methylated DNA binding protein-2-H1 (MDBP-2-H1) consists histone H1 subtypes which are truncated at the C-terminus.";
Nucleic Acids Res. 25:5052-5056(1997).
-I- FUNCTION: Histones H1 are necessary for the condensation concleosome chains into higher order structures.
-I- SUBCELIULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1988 (Rel. 08, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Histone H1.10 (Methylated DNA binding protein-2-H1) (MDBP-2-H1)
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H110 CHICK
P08286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coles L.S., Robins A.J., Madley L.K., Wells J.R.E.; "Characterization of the chicken histone H1 gene complement Generation of a complete set of vertebrate H1 protein sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87250632; PubMed=3597432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                          DENTIFICATION OF ALA-13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol.
s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EWBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
                                                                                                                                                          SIMILARITY: Belongs to the histone H1/H5 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ekkraokadeakrreeralkeerdrltaeaskoaaakakkaaesaaklaassallasaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Missing (In isoform E).
/FTId=VSP_004052
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/KSSYSPIYSSYSVPRRYYGATRVVTSPIRVVTSPARVVSRV
IHSPSPRVVHRTTTKVISPER -> SIWFSSLSPTSLVII
HLSMDYYYSFLLTYITHCSITSITSSSLEKQIRLVISPHII
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DPVTAFGVRRPDLERRQRSILDPINRASIKPDYKLAYEPIE
PYVSTRDKNRIRILGMVRQHIDTVEAGGNTAGRTFRDSLDA
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4507369593D1DD3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 AA
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HSSP; P08287; 1GHC.
InterPro; IPR005818; Histone_H5.
InterPro; IPR005819; Histone_H5.
Pfam; PF00538; Iinker histone; 1.
PRINTS; PR00624; HISTONEH5.
SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage by are entitles requires a license.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yelton D.B., Limberger R.J., Curci K., Malinosky-Rummell F., Sliviensky L., Schouls L.M., van Embden J.D., Charon N.W., "Treponema phagedenis encodes me expresses homologs of the pallidum TmpA and TmpB proteins.", Infect. Immun. 59:3685-3693(1991).
                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
    REPEAT
                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).

    -!- SUBCELLULAR LOCATION: Outer membrane-associated
    -!- SIMILARITY: TO TMPB OF T.PALLIDUM.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treponema phagedenis.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P29720;
01-APR-1993
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                                                 DOMAIN
                                                                                            SIGNAL
                                                                                                                                                           PIR; B43592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91372983; PubMed=1894368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treponemal membrane protein
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INIT MET
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                                                                                                                                        InterPro;
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                                                                                                                                    IPR008941; TPR-like.
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Pred. No. 0.0001;
                                            TREPONEMAL MEMBRANE PROTEIN 17 X 5 AA TANDEM REPEATS OF
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precursor (Antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Length 219;
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RESULT 12
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28-FEB-2003
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384 AA;
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Biochemistry 32:11345-11351(1993).

-I- FUNCTION: Histones H1 are necessary for the cond nucleosome chains into higher order structures.
-I- SUBCELLULAR LOCATION: Nuclear.
-I- SIMILARITY: Belongs to the histone H1/H5 family.
                                                                                                     MEDLINE-94032251; PubMed-8218199;
Cerf C., Lippens G., Muyldermans S., Segers A
Wodak S.J., Hallenga K., Wyns L.;
"Homo- and heteronuclear two-dimensional NMR
                                                                                                                                                                                                         MEDIINE=87250632; PubMed=3597432;
Coles L.S., Robins A.J., Madley L.K., Wells J.R.E.;
"Characterization of the chicken histone H1 gene complement
"Characterization of a complete set of vertebrate H1 protein sequer
                                                                                                                                                                                                                                                                                                                   Gallus garrus Chordata, C
Eukaryota; Metazoa; Chordata, C
                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
                                                                                       domain of histone H1: sequential
                                                                                                                                                               STRUCTURE BY NMR OF 40-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 KAKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAKEAAY 107
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                                                                                                                                                                                            Chem. 262:9656-9663(1987).
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(Rel. 08, Last seq
(Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243
252
270
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288
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Neognathae; Galliformes; Phasianidae; Phasiani
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Last annotation updat
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1-17.
6 X 8
A-A-E.
2-1.
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1-11.
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                                                                                                                                 Segers A., Ramakrishnan
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                                             for the condensation
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                                                                                        secondary
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                                                                                                     of the
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RESULT
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Best Local (
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STANDARD; PRT; 206 AA.
P06350; P83374;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update).
15-MAR-2004 (Rel. 43, Last annotation update).
H15-MAR-2004 (Rel. 43, Last annotation update)
H16tone H1 [Contains: Oncorhyncin II].
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
                                                          SEQUENCE OF 138-154, FUNCTION OF ONCORHYNCIN II, AND MASS SPECTROMETRY OF 138-206.
TISSUE-Skin mucus;
MEDLINE=22850086; PubMed=12969798;
MEDLINE=22850086; PubMed=12969798;
MEDLINE=22850086; PubMed=12969798;
MEDLINE=20850086; PubMed=12969786; PubMed=12969788;
MEDLINE=20850086; PubMed=12969788;
MEDLINE=20850086; PubMed=12969788;
MEDLINE=20850086; PubMed=12969788;
MEDLINE=20850086; PubMed=12969788;
MEDLINE=20850086; PubMed=12969788;
MEDLINE=20850086; PubMed=12969788;
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                               Oncorhynchus mykiss."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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PRINTS; PR00524; HISTONEH5.
SMARF; SM00526; HIS; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=85264847; PubMed=6443128;
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InterPro; IPR005819; Histone_H5.
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                                                                                                                                                                                                                                                                                                                                                                                                                Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                quita J., Connor W., Winkfein R.J., H1 histone gene from rainbow trout Mol. Evol. 21:209-219(1985).
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Immunol. 28:127-138(2004).
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Pred. No. 0.00014;
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Best Local (
                                                                                                                                                                                                                                  H15_HUMAN STANDARD; PRT; 225 AA. P16401; Q14529; 01-AUG-1990 (Rel. 15, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Histone H1.5 (Histone H1a).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SITE
SEQUENCE
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                             "Human spleen histone H1. Isolation and amino acid sequences of three minor variants, H1a, H1c, and H1d."; J. Blochem. 106:844-857(1989).
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                                                                                 Ohe Y., Hayashi
                                                                                                  TISSUE=Spleen;
MEDLINE=90130391; PubMed=2613692;
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ł
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                       Homo sapiens (Human).

Rukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
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SEQUENCE FROM N.A.
                                                                                                                                     SEQUENCE
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InterPro; IPR005819; Histone H5.
Pfam; PF00538; linker histone; 1.
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                                                                                                                                                                     NCBI_TaxID=9606;
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INIT_MET 0 0
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FUNCTION: Oncorhyncin II has antibacterial activity against Gram-
positive and Gram-negative bacteria at submicromolar
concentrations. Potentially important role in mucosal defense.
SUBCELLULAR LOCATION: Nuclear. Oncorhyncin II is secreted.
TISSUE SPECIFICITY: Oncorhyncin II is expressed in skin.
MASS SPECTROMETRY: MM=7195.3; METHOD=MALDI; RANGE=138-206.
MISCELLANEGUUS: Is thermostable up to 80 degrees Celsius.
SIMILARITY: Belongs to the histone H1/H5 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Histones H1 are necessary
                                                                                                                                                                                                                                                                                                                                                                                                                                     165 VKKPA--AAAK---KAAKSPKK---ATKAAKPKAAKPKAAKKAAPKK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105
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ACETYLATION (BY SIMI
GLOBULAR.
CLEAVAGE (PROBABLE).
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Pred. No. 0.00019;
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                                                                                                                            RESULT 15
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Best Local
        Q9ZHC5;
16-OCT-2001
16-OCT-2001
10-OCT-2003
DNA-binding
                                                                                                             MYCSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0000786; C:nucleosome; NAS.
GO; GO:0003677; F:DNA binding; NAS.
GO; GO:0003677; F:DNA binding; NAS.
GO; GO:0000607; P:Chromosome organization and biogenesis (sen. . .; NAS.
GO; GO:0006334; P:nucleosome assembly; NAS.
InterPro; IPR005818; Histone_H1/H5.
InterPro; IPR005819; Histone_H5.
Pfam; PF00538; linker_histone; 1.
PRINTS; PR00624; HISTONEHS.
SMART; SM00526; H15; 1.
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                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF531304; AAN06704.1; -.
EMBL; Z98744; CAB11421.1; -.
PIR; S51660; S51660.
HSSP; P08287; 1GHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22296985; PubMed=12408966; Marzluff W.F., Gongidi P., Woods K.R., Jin J., Maltais L.J.; "The human and mouse replication-dependent histone genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97183654; PubMed=9031620;
Albig W., Meergans T., Doenecke D.;
"Characterization of the H1.5 gene completes the set of human H1
subtype genes.";
                                                                                          DBH_MYCSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X83509; CAA58498.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- FUNCTION: Histones H1 are necessary for the condensation nucleosome chains into higher order structures.
-i- SUBCELIULAR LOCATION: Nuclear.
-i- SIMILARITY: Belongs to the histone H1/H5 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:4719; HIST1H1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomics 80:487-498(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 184:141-148(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        118
                                                                                                                                                                       176 AKAAAKPKKATKSPAKPKAVKPKAAKPKAAKPKAAKPKAAKKAAAKK 224
                                                                                                                                                                                                        56 АККЕЛҮКЛЕЛККҮЛКЛАКАЕККЕҮЛЛЛЕЛККАЕЛЛКАҮКЛЕЛАКЛАЛКЕ 104
                                                                                                                                                                                                                                                                                                        51;
                                                                                                                                                                                                                                                                       1 АККУАККАЕКАУАККАККАКЕККАУАККЕАКАУКАА----ЕАКККАКАЕАККУАКЕЛАК 55
                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                       AKPKAKKAGAAKAKKPAGATPKK--AKKAAGAKKAVKKTPKKAKKPAAAGVKKVAKSPKK
                                                                                                                                                                                                                                                                                                                                                                  0
1
215
225 AA;
          protein
           (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 42, Last annotation update)
protein HU homolog (Histone-like)
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                 0
1
217
22449 MW;
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MISSING (IN REF. 1).
, 26CD4A1E5D463CDA CRC64;
                                                                                                                                                                                                                                                                                                                     Score 160.5; DB Pred. No. 0.00021
           (Histone-like protein) (Hlp).
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                                                                                            208
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                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                     Length 225;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding; DNA condensation; Repeat.

DOMAIN

1 90 BACTERIAL HISTONE-LIKE DOMAIN.

DOMAIN

101 205 DEGENERATE REPEATS REGION.

SEQUENCE 208 AA; 21230 MW; CA5F577F61F7EF09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00216; Bac_DNA_binding; 1.
PRINTS; PR01727; DNABINDINGHU.
ProDom; PD000945; Bac_DNAbind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF068138; AAD13809.1; -. HSSP; P02346; 1HUU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: Histone-like DNA-binding protein which is capable of
wrapping DNA to stabilize it, and thus to prevent its denaturation
under extreme environmental conditions (By similarity).
-!- SIMILARITY: Belongs to the bacterial histone-like protein family.
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NCBI TaxID=1772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium smegmatis.
Bacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00411; BHL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=ATCC 700084 /
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"Upregulation of a histone-like protein in dormant Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99110209; PubMed=9894918;
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162
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                                                                                                                                                    AKKAAKKAP---AKKAAAKKTATKAAAKKAPAKKAA----TKAPAKKAATK-APAKKAA 161
                                                                                                                                                                                                                                 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60
                                                                                                                                                                                                                                                                                                                 Conservative
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.; 21230 MW;
                                                                                                                                                                                                                                                                                                                                             30.8%;
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Pred. No. 0.
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Search Job tim rch completed: April 20, time : 15.8636 secs 2004, 23:16:19

HUP OR HLP

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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519
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1: sp_archea:*
2: sp_bacteria:*
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                                                                          sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_phage:*
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sp_mammal:*
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# SUMMARIES

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168.5	170	170.5	173.5	176.5	176.5	178	178	178	181.5	184.5	188.5	190.5	190.5	190.5	202	Score
32.5	32.8	32.9	33.4	34.0	34.0	34.3	34.3	34.3	35.0	35.5	36.3	36.7	36.7	36.7	38.9	Query Match
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Q8F140 Q7WFN5 Q90ZD7 Q8EHL5	Q9AT23 Q81UR6 Q8LKI1 Q9AT20 Q9AT24 Q9AKG7	Q45370 Q87Y39 Q82KM1 Q26947 Q9KR10 Q9KR10 Q9KR10 Q9LKH19 Q8LKH10 Q8LK10 Q9Z722 Q9Z722 Q9Z720 Q9Z721	Q7W3X2 Q39598 Q34528 Q84528 Q7VUT9
Q9D140 xanthomonas Q7wfn5 bordetella Q90zd7 bufo bufo g Q8ehl5 shewanella	pisum sabacillus lathyrus cul lens cul pisum sapisum sarhizobiu	Q45370 bordetella Q87y39 pseudomonas Q82kml streptmyce Q26947 trypanosoma Q9kr10 vibrio chol Q9at18 lens culina Q81ki0 pisum fulvu Q81ki0 pisum sativ Q9at22 lathyrus sa Q9zr20 pisum sativ Q9at21 lathyrus sa Q9zr20 pisum sativ Q9at21 lathyrus sa Q81hj4 bacillus ce Q9at25 pisum sativ Q88ze7 lactobacill	Q7w3x2 bordetella Q39598 chlamydomon Q84528 paramecium Q7vut9 bordetella

#### ALIGNMENTS

AC Q937K4 DT 01-DEC-2001 (TrEMBL DT 01-DEC-2001 (TrEMBL DT 01-DEC-2003 (TrEMBL DT 01-OCT-2003 (TrEMBL DT 01-OCT-2003 (TrEMBL DE TOLA, OS Erwinia chrysanthem OC Bacteria; Protecbac OC Enterobacteriaceae; OX NCBI_TaxID=556; RN [1] RP SEQUENCE FROM N.A. RC STRAIN=3937; RA RAY M.C., Vianney A RT "characterization o RL SUBmitted (OCT-2000 DR EMBL; AUJ97885; CAC SEQUENCE 395 AA; Query Match Best Local Similarity Matches 62; Conserv Matches 62; Conserv 1 AKKYAKKAEK Db 138 AKEQKOAEV OY 44 ABAKKYAKEA Db 199 KAAAKEAAYE OY 99 KAAAKEAAYE Db 198 KKAAAATAAKQ OY 99 KAAAATAAKQ OY 99 KKAAAATAAKQ	
EC-20 EC-20 CT-20 CT-20 For the restriction of the	RESULT Q937K4 ID Q
Birel. 19, Created) Birel. 25, Last sequalized. 25, Last annotered.  acteria; Gammaproteces; Pectobacterium.  A., Cotte-pattat N. of the Erwinia chry cotte State Chry 1600 to the EMBL/GenE 1600 MW; 3 COCII 38.9%; Score 20, 47.3%; Pred. NG Cryative 15; Misma SKAYAKKAKAAKE 15; Misma SKAYAK	LT 1 K4 Q937K4 PRELIMINARY; PRT; 395 AA.

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Best Local :
                                                     Q88NI6;
01-JUN-2003
01-JUN-2003
           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat Biopolymer transport protein TolA. TOLA OR PP1221.
                                                                                                                                                                                                                                                                                                                                                                                          Rodriguez-Herva J.J., Ramos J.;
"Characterization of an Oprl null mutant of Pseudomonas putida.";
J. Bacteriol. 178:5836-5840(1996).
EMBL; X74218; CAB50780.1; -.
GO; GO:0000786; C:nucleosome; IEA.
GO; GO:0005534; C:nucleosome; IEA.
GO; GO:0005534; P:DNA binding; IEA.
GO; GO:000534; P:DNA binding; IEA.
GO; GO:000534; P:DNA binding; IEA.
GO; GO:000534; P:DNA binding; IEA.
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InterPro; IPR006260; TonB C.
PRINTS; PR00624; HISTONEH5.
TIGREPAMS; TIGR01352; tonB Cterm; 1.
SEQUENCE 372 AA; 40133 MW; 87F49785ECC3C0BC CRC64;
Pseudomonas putida (strain KT2440)
                                                                                             91N88D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rodriguez-Herva J.J.;
Submitted (JUL-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                xoariguez-Herva J.J., Ramos-Gonzalez M.I., Ramos J.;
"The Pseudomonas putida peptidoglycan-associated outer membrane
lipoprotein (PAL) is involved in maintenance of the integrity of
cell envelope.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas putida.
Bacteria; Proteobacteria; Gammaproteobacteria;
Pseudomonadaceae; Pseudomonas.
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01-NOV-1999 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96422022; PubMed=8824639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ramos-Gonzalez I.;
Submitted (JUN-1995)
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                                                                                                                                                                 177
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                                                                                                                                                                                                                                            AKKAEKAYAKKAKAAK----EKKAYAKKEAKAYKAAE-----AKKKAKAEAKKYAKEAA
                                                                                                                                                              KKAAAEEAKKKAAEDAKKKAAEEAKKKAAEDAKKKAAAEDAKKKAAEEAKKKAAADA 233
                                                                                                                                                                                                                                                                         Conservative
                                                                                               PRELIMINARY;
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Last annotation update)
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01-JUN-2002
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Melson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Melson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Brinkac L., Beanan M., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                   "Evolutionary relationships of conserved cysteine-rich motifs adhesive molecules of malaria parasites.";
Mol. Biol. Evol. 0.0-0(2002).

EMBL; AV042083; AALI0508.1;
Interpro; IPRO08602; Duffy_binding.
Pfam; PF04244; Duffy_binding; 1.
SEQUENCE 1866 AA; 212420 MW; DC692D7CFAE7D93F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGE;
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GO; GO:0000786; C:nucleosome; IEA.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0003673; P:nucleosome assembly; IEA.

InterPro; IFR005819; Histore—H5.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Michon P., Stevens J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium vivax
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                                                                                                                 Conservative
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                                                                                                           36.7%; Score 190.5; DB 5;
49.6%; Pred. No. 4.1e-05;
tive 17; Mismatches 22;
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Pred. No. 9.
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RESULT 6

Q8ZQT6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8ZQT6
Q8ZQT6;
Q1-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 23,
                               STRAIN-LT2 / SGSC1412 / ATCC 700720;

MEDLLINE=21534948; PubMed=11677609;

McClelland M., Sanderson K.E., Spieth J., Clifton S.W.,

McClelland M., Sonderson K.E., Spieth J., Clifton S.W.,

Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou

Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., M

Leonard S., Nguyen C., Miller W., Stoneking T., Nha

Machantan Willer W., Stoneking T., Nha
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria;
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01-OCT-2003
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Enterobacteriaceae; Escherichia
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53.0%;
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                                            Stoneking T., Nhan M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterobacteriales;
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                                                                           .W., Latreille P.,
Hou S., Layman D.,
N., Mulvaney E.,
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120 AEEAAKQAELKQKQAEEAAAKAAADAKAKAEADDKA--AEEAAKKAAADAKKKAEAEAAK 177

56 AKKEAY-KAEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAKAAAKEAA 106

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QBX965
ID QBX965
ID 01-M
QBX967
AC QBX9
AC QBX9
AC QBX9
AC QBX9
AC OL-M
ODT 01-M
ODT 01-M
DT 01-M
DT 01-M
OC Bacch
OC Bacch
OC STRA
AC STRA
RX MEDL
RA ROSSE
RA ROSSE
RA Weelc
RA Pern
RA Weelc
RA Pern
RA Weelc
RA Post
RA WEDL
RA Haya
RA Haya
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                                                                                     Query Match
Best Local
                                                              Matches
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TOLA OR Z0907 OR ECS0774.

Bscherichia coli O157:H7.

Bacteria: Protection:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhaw G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R., "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.", Nature 409:529-533(2001).
                                                                                                                                                                                                                        EMBL; AB005252; AAG55075.1; -.
EMBL; AP00253; BAB34197.1; -.
PIR; F90725; F90725.
PIR; G85576; G85576.
                                                                                                                                                                                                                                                                                                                                                          MEDIINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoy;
Hayashi T., Makino K., Ohnishi M., Murata T., Tanaka M., Tobe 'Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Yasuna;
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasuna;
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
"Complete genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-CCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE008730; AA Complete proteome. SEQUENCE 407 AA;
                                                                                                                                                                     SEQUENCE 394 AA;
                                                                                                                                                                                                                                                                                                                                           DNA Res. 8:11-22(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=0157:H7 / F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
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STRAIN=0157:H7 / E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 EAAKAAAEAKKKAEAEAAK----AAAEAKKKADAEAAKA-AAEAKKKADAAAAKAAAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138
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                                                        60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 EAYK--AEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAK---AAAKEAAYEA
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  1 АККУАККАЕ----КАУАККАКААКЕККАУАККЕАКАУКААЕАКККАКАЕАККУАК-ЕААК 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYK-AAEAKKKAKAEAKKYAKEA-AKAKK 58
                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 AA; 41865 MW;
                                                              Conservative
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                                                                                                                                                                           40517 MW;
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                                                                                     52.2%;
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                                                                                  Score 181.5; DB Pred. No. 4e-05;
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Pred. No. 2.
                                                                                                                                                                        5B58D8E8230BDE28 CRC64;
                                                        Mismatches
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                                                                                                                DB 16;
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                                                           32;
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                                                           Indels
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                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yokoyama K.,
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                                                           Gaps
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RESULT 9
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Q8Z8C1
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Best Local S
Matches 58
                                                                                                                                                                                                                                                               Q8ZGZ2;
Q8ZGZ2;
01-MAR-2002
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Q8Z8C1;
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel 20, Created)
01-MAR-2002 (TrEMBLrel 20, Last sequence update)
01-JUN-2003 (TrEMBLrel 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
NCBI_TaxID=632;
[1]
                                                        Enterobacteriaceae; Yersinia.
                                                                 Yersinia pestis.
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                         Tola colicin import membrane TOLA OR YPO1123.
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SEQUENCE 376 AA; 38804 MW; EC21F2C4767A8A42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 185:2330-2337(2003).
EMBL; AL627268; CAD05209.1; -.
EMBL; AE016841; AAO69743.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=TY2 / ATCC 700931;
STRAIN=Ty2 / ATCC 700931;
MEDLINE=25231367;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi st.
and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STY0793 OR TOLA OR T2129.
Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21534947; PubMed=11677608;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (F)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAA---KEAAYE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -KAEAEAAKAAADAKKKADAEAAKAAAEAKKKADAAAAKAAADAKKKAAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKAAADAKKKAEAEAAKAAADAKKKAEAEA-AKAAADAKKKAEAEA---AKAAAEAKK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.3%; Score 178; DB 16;
52.3%; Pred. No. 6.6e-05;
tive 10; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                       388 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
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                                                                                    Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yersinia pestis.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=KIM5 / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
MEDLINE=22137863; Plunkett G. III, Boutin A., Mayhew G. Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G. Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., E. Berry, P. Derry, P. D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
Membrane spanning protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=632;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8CZZ8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ414146; CAC89966.1; -. PIR; AC0138; AC0138.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=CO-92 / Bio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perry R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                          145 KQAABQQKIAAAAVAKAKBEQKQABTAAAQAKABADKIVKAQABAQKKABABAKKBAAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 A 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 AAAKKQA-DADAKKAVEVAEKAAADAAEKKAAADAE-KKAAAAKKVAAAAEAKKKAAAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 KQAAEQQKIAAAAVAKAKEEQKQAETAAAQAKAEADKIVKAQAEAQKKAEAEAKKEAAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AE013906; AAM86606.1;
                                                                      54 АКАККЕАУКАЕАККУАКААК------АЕККЕУАААЕАККАЕААК--АУКАЕААКАААКЕА 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 AKAKKEAYKAEAKKYAKAAK-----AEKKEYAAAEAKKAEAAK--AYKAEAAKAAAKEA 105
                                                                                                                                                                                                                                          2 KKYAKKAEKAYAKKAKAAKEKK-----AYAKKEA-KAYKA-AEAKKKAKAEAKKYAKEA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63;
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                                                                                                                                                                                                                                                                                                                                                                          Similarity
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AAAKKQA-DADAKKAVEVAEKAAADAAEKKAAADAE-KKAAAAKKVAAAAEAKKKAAAEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        393 AA; 41012 MW; 1E3E4FF87E533481 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              388 AA;
                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                     34.3%; Score 178; 52.1%; Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.3%; Score 178; DB 16; 52.1%; Pred. No. 6.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                     ; pred. No. 6.9e-05; 12; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .'
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                                                                                                                                                                                                                                                                                                                                                                                                             DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16;
                                                                                                                                                                                                                                                                                                                         28;
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 393;
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                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                             18;
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Q8XVN7
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Best Local S
Matches 67
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A Arlat M., Billault A., Brottler P., Camus J.C., Cattolico L.,
A Arlat M., Billault A., Brottler P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
A Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
A Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
Weissenbach J., Each Plant pathogen Ralstonia solanacearum.";
Weissenbach J., Each Plant pathogen Ralstonia J., Cantolico J., Cantolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 200 AA;
STRAIN=301 / Serotype 2a;
                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                        Shigella flexneri.
                                                                                                                                                                                                                                                            Membrane spanning protein,
TOLA OR SF0558 OR S0571.
                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25, probable histone H1 protein. RSC2793 OR RSO0453.
                                                                                                          NCBI_TaxID=623;
                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q83SA1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burkholderiaceae; Ralstonia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8XVN7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKKVA--AKKVAAKKAPAAKKAAVKKVAAKKAAPAKKAAVKKVAAKKAPAAKKAAVKKVA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKKYAKKAEKAYAKKAKAAKE---KKAYAKKEAKAYKAAEAK---KKA----KAEAKKY-
                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 24,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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, Last annotation update)
required for outer membr
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Pred. No. 4.7e-05;
5; Mismatches 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413 AA.
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RESULT 13
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Best Local :
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9CM70;
                                                                                                                                         InterPro; IPR000533; Tropomyosin. PRINTS; PR00194; TROPOMYOSIN. Complete proteome.
                                                                                                                                                                                                                          May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., K "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gam
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE=22590274; PubMed=12704152; Wei Jr. Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Wei Jr., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier Gr., Mayhew G.F., Plunkett G. III, Rose D.J., Darling J. Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R., "Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T"; Infect. Immun. 71.2775.2786 (2003)."
                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               Pasteurella multocida.
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002
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EMBL; AE016979; AAP16075.1; -.
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                                                                                                                                                                                                HSSP; P19934; 1TOL
                                                                                                                                                                                                                                                                             MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22272406; PubMed=12384590;
                                                                                                                                                                                                                                                                                                                                             CBI_TaxID=747;
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 145 KQAEEAKAKQLAEAAKLKAEAEAKRLAALAKQAEEEEAKAKAAEEAKRKAEKAKAEAEAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 OKKAEVAAAALKKKAEAAEAAAAEARKKAATEAAEKAKAEAEKKAAAEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 KKQAEEAAKQAELKQKQAEVAAAKAAADAKA--AEEAAKKAAADAKKKAEAEAAKAAAEA 174
                                                                                                                                                                                                                AE006136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 У-КАБАККУАКААКАБККЕУАААБАКК---АБААКАУКАБААКАААКБАА 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57;
                               6 KKAEKAYAKK-AKAAKEK-KAYAKKEAKAYKAAEAKKKAKA--EAKKYAKEA----AKA 56
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                                                                                                                                389 AA; 42197 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.
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                                                                                                                                                                                                                AAK03052.1; -.
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                                                                                 33.4%; Score 173.5;
48.7%; Pred. No. 0.0
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17,
22,
                                                                                                                                                                                                                                                                                                                                                                            Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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Pred. No. 9.1e-05;
                                                                                                                                B4032F2A2FD9E94B CRC64;
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204
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RESULT

ID 9576

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Best Local S
Matches 54
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Q39576;
Q1-NOV-1996
Q1-NOV-1996
Q1-OCT-2003
Histone H1.
CH1.
                                         88888
                                                                                                                                                                                                      MEDITINE=96120862; PubMed=8590479; Fabry S., Muller K., Lindauer A., Park P.B., Cornelius T., Schmitt R. Fabry S., Muller K., Lindauer A., Park P.B., Cornelius T., Schmitt R. "The organization structure and regulatory elements of Chlamydomonas histone genes reveal features linking plant and animal genes."; histone genes reveal features linking plant and animal genes."; Curr. Genet. 28:333-345(1995).

EMBL; U16726; AAA98452.1; -.

EMBL; U16726; AAA98452.1; -.

EMBL; U56726; AA99452.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydomonas reinhardtii.
Bukaryota; Viridiplantae; Chlorophyta;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99115903; PubMed=9448314;
Kappe S.H.I., Noe A.R., Fraser T.S., Blair P.L., Adams J.
"A family of chimeric erythrocyte binding proteins of mal
parasites.";
Proc. Natl. Acad. Sci. U.S.A. 95:1230-1235(1998).
EMBL, AF031886; AAC05366.1; -.
EMBL, F031886; AAC05366.1; -.
PIR; T09127; T09127.
InterPro, IPR036802; Duffy binding.
Pfoam; PF05424; Duffy binding; 1.
SEQUENCE 1701 AA; 199268 MW; EDABEZDEFD87CE8A CRC64;
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01-AUG-1998 (TREMBLrel. 07, Last sequence update)
01-OCT-2003 (TREMBLrel. 25, Last annotation update)
Erythrocyte binding protein.
MAEBL.
                                                                                                                                                                                    HSSP;
              InterPro;
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Eukaryota; Alveolata; Apicomplexa;
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P; P02259; IHST.
G0:0000786; C:nucleosome; IEA.
G0:0005634; C:nucleos; IEA.
G0:000567; F:DNA binding; IEA.
G0:000367; F:Chromosome organization and biogenesis (sen. . .;
G0:0007001; P:chromosome assembly; IEA.
G0:0006334; P:nucleosome assembly; IEA.
erPro; IPR005818; Histone_H1/H5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERKKKAEAAKKAEEKKKAEAAKKAEEE 1301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 25,
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Best Local &
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InterPro; IPR003216; Linkerhist N.
Pfam; PF00538; linker histone; T.
PRINTS; PR00624; HISTONEH5.
ProDom; PD000373; Linkerhist N; 1.
SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                         SEQUENCE
 220
                                104 EAA 106
                                                                160 АЕККРКААКРАККТРТККАЛАКРКАЕККРКААКРКАЕККРКААКРКАЕККАКЛАКРААК 219
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Search completed: April 20, 2004, 23:17:46 Job time: 52.961 secs

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A_Geneseq_29Jan04:*
1: geneseqp1980s:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result No. 1 2 3	31 10 31 10 22 28 5 20 9	Query Match 100.0 60.2 55.7 44.0	Length 109 86 77 66	23334	5	Description Aay82577 Co Aay82576 Co Aay82575 Co Aay82575 Co Aay82574 Co Aar06445 Re
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present inventions the molecular weight invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

WPI; 2000-317499/27.

Claim 10; Page 14; 72pp; English.

162 31.3 64 ABU42038 162 31.3 643 ABU42038 162 31.2 356 ABU49418 162 31.2 356 ABU49418 162 31.2 356 ABU49418 162 31.2 356 ABU49418 160.5 30.9 158 2 AAY37366 160.5 30.9 158 2 AAY37366 160.5 30.9 226 2 AAY3738 160.5 30.9 226 2 AAY3738 160.5 30.9 226 2 AAY3738 160.5 30.9 226 ADA35034 159.5 30.7 234 AADA35034 159.5 30.7 234 AADA3294 159.5 30.7 234 AADA3284 159.5 30.7 234 AADA3284 159.5 30.7 234 AADA3284 159.5 30.7 234 AADA3284 159.5 30.7 234 AADA32892 158.5 30.7 234 AADA32892 158.5 30.4 218 2 AAY374034 159.5 30.4 218 2 AAY374034 159.5 30.3 564 2 AAY374034 159.5 30.3 564 2 AAY374034 159.5 30.3 564 2 AAX3382	331.2 33	45	44	43	42	41	40	39	38	37	36	<b>3</b> 5	34	u u	32	<u>u</u>	30	29	28	27	26
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### ALIGNMENTS

AAY82577 standard; peptide; 109 AA.

Copolymer; molecular weight marker; TV-marker; immune disease; glatizamer acetate; autoimmune disease; antitarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsortatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; croin's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; Gad A, Lis D; 25-SEP-1998; 06-APR-2000. Unidentified. AAY82577; (YEDA ) YEDA RES & DEV CO LTD (TEVA-) TEVA PHARM USA INC. 24-SEP-1999; WO200018794-A1. pemphigus vulgaris; systemic lupus erythematosus. Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7. 28-JUL-2000 (first entry) 98US-0101693P. 99WO-US022402

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RESULT 2
AAY82576
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Best Local S
Matches 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copolymer; molecular weight marker; TV-marker; immune disease; glatizamer acetate; autoimmune disease; antiarthritic; neuroprofective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidiabetic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; nembirals in the state of the 
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                                                                                                                                             25-SEP-1998;
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(YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
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Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

WPI; 2000-317499/27.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura. Colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological;
                                                                                  25-SEP-1998;
                                                                                                                                                                    24-SEP-1999;
                                                                                                                                                                                                                                                           06-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-2000 (first entry)
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    (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                     WO200018794-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY82571 to AAY82577 represent specifically claimed copolymer molecular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    molecular weight TV-marker amino acid sequence SEQ ID NO:5
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                                                                                  98US-0101693P.
                                                                                                                                                                    99WO-US022402.
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72.1%;
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Pred. No. 3.9e-19;
1; Mismatches 3
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AN ANY82571 to ANY82577 represent specifically claimed copolymer molecular CC weight TV-marker polypeptides from the present invention. The present cc invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an CC amino acid composition corresponding to the copolymer. The polypeptides CC in the invention are used as molecular weight markers for glatiramer CC acetate related tetrapolymers. The polypeptides may also be used for CC treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated CC diseases. Such diseases include arthritic conditions, demyelinating CC diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoric contribis, osteoarthritis, autoimmune uvecertinitis, Crohn's CC disease, Chronic immune thyroiditis, autoimmune uvecertinitis, Crohn's CC disease, Chronic immune thyroiditis, autoimmune uvecertinitis, Crohn's CC syndrome, Hashimoto's disease, didopathic myxoedema, myasthenia gravis, CC syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, CC psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated disease which can be treated include host-versus-graft disease, CC graft-versus-host disease, and delayed-type hypersensitivity. The CC graft disease, and delayed-type hypersensitivity and physical properties which are analogous to glatiramer acetate molecules, which can makes them ideal for use as molecular weight markers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                           Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarrhritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; mysathenia gravis;
                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 77 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                  Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY82574 standard; peptide; 66 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gad A,
                                                                                           pemphigus vulgaris; systemic lupus erythematosus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 -KAEAKKYAKAAKAEKKEYAAAEAK-----YKAEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 УКАЕАККУАКААКАЕККЕУАААЕАККАЕААКАУКАЕААКАААКЕААУЕА 109
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Pred. No. 3.1e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3; Length 77;
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WO200018794-A1.

Synthetic.

Recombinant

mmunological

copolymer 1; COP-1-77; myelin basic protein; MBP; al activity; autoimmune encephalomyelitis; multiple sclerosis.

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AAR06445
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                                                                                                                                                                                                                                                           RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      actate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating conditions, demyelinating autoimmune there is autoimmune the autoimmune haemolytic anaemia, autoimmune coophoritis, autoimmune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, craves disease, dislated sensitivity disease, disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated disease, and delayed-type hypersensitivity. The collipse coplypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which can be treated include host-versus-graft disease, and delayed-type hypersensitivity. The coplyperties which are analogous to glatiramer acetate molecules, which
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 66 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gad A,
                                                                                                Recombinant copolymer 1-77, myelin basic protein analogue.
                                                                                                                                    25-MAR-2003
03-JAN-1991
                                                                                                                                                                                    AAR06445;
                                                                                                                                                                                                                         AAR06445 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-317499/27
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                                                                                                                                                                                                                                                                                                                                           61 YKABAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       62;
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                                                                                                                                                                                                                                                                                                             -KAEAKKYAKAAKAEKKEYAAAEAK-----YKAEAAKAAAKEAAYEA
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                                                                                                                                                                                                                        protein; 154
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Pred. No. 3e-12;
D; Mismatches
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RESULT 6
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XX ABU4
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DT 19-J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC To improve the expression of rCOP-1 polypeptides in E. coli, genes coding CC for rCOP-1-77 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-CC MOV-1984 US4691009, NRRL B-15910), a plasmid used to express Protein A. CC The resulting plasmids encode fusion proteins consisting of beta-cc cocurs between the Protein A, and rCOP-1 sequences. A methionine residue cocurs between the Protein A and rCOP-1 sequences, originating from the CC cocurs between the Protein A and rCOP-1 sequences, originating from the first on protein. rCOP-1-77 contains oligonucleotide duplexes incoding the following segments: YKK, EAE, KAK, AAK, and AAA. The N-CC terminal alanine residue is left behind following CNBr cleavage of the fusion protein. The product prevents or arrests experimental autoimmune coc demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in certain amino acids. See also AAQ05665. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local |
                                                                                                              Protein encoded by Prokaryotic essential gene #25712.
                                                                                                                                                                                                             ABU40185 standard; protein; 372 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cook
                                               Pseudomonas putida
                                                                                Antisense;
                                                                                                                                                  19-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or immunological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-FEB-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                    142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                    KYKKEAEK--AKEA 153
                                                                                                                                                                                                                                                                                                                                  AYKAEAAKAAAKEA 105
                                                                                                                                                                                                                                                                                                                                                                 EYKKKAKAAAEAEYKKEAEEAEYKKYKKKAKKAKYKKKAKEAEKAKAAAEAEKAKEAEYK 141
                                                                                                                                                                                                                                                                                                                                                                                                 EAKKYAKEAAKA--KKEAYKAEAKKYAKAAKAEK-----KEYAAAEAKKAEAA--K 91
                                                                                                                                                                                                                                                                                                                                                                                                                                 KKKAKEAEKAKKAKYKKYKKEAEAAKAAKAAAAAYKKEAEA--AAEAEKAKYKKKAKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKYAKKAEKA-----YAKKAKAAKEKKAYA----KKEAKAYKAAEA-----KKKAK-A 44
                                                                                prokaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.3%;
                                                                                essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 209; DB 2;
Pred. No. 3.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                               gene; cell proliferation; drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 81
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WO200277183-A2

RESULT 7 ABU27824

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                                                                                                                                                                                                                                                                                      CC encoding a polypeptide whose expression is inhibited by the antisense culletic acid; (2) a host cell containing the vector; (3) an isolated compounding a polypeptide whose expression is inhibited by the antisense compounding the vector; (3) an isolated compounding the vector; (3) an isolated compounding the polypeptide; (6) inhibited by the compounding the polypeptide; (6) inhibited by the compounding the polypeptide; (6) inhibiting cellular compounding the polypeptide; (7) identifying a compound that influences the activity of compounding the proliferation, or that inhibits cellular proliferation, (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits and compound the strains is present in a culture or collection of compounding the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the collection of an organism. The antisense mucleic acids are useful for cellular proliferation to isolate candidate molecules for rational cord discovery programs, or for screening homologous mucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, compound that inhibits the collection of the target prokaryotic essential genes. Note: The sequence data for this carent did not form part of the printed specification, but was obtained content form this part of the printed specification, but was obtained content in the printed specification.
                                                                                                                                                                                         Matches
                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                   Sequence 372 AA;
                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; SEQ ID NO 68109; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e 6213 antisense sequences given in the specification where expression the nucleic acid inhibits proliferation of a cell. Also included are:

a vector comprising a promoter operably linked to the nucleic acid
                                                                                                                                                                                         59;
                                                                                                                                       5 АККАЕКАУАККАКААК----ЕККАУАККЕАКАУҚААЕ-----АКККАКАЕАККУАКЕАА 54
                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELITRA PHARM INC.
KKAAAEEAKKKAAEDAKKKAAEEAKKKAAEDAKKKAAAEDAKKKAAEEAKKKAAADA 233
                                                                                          AKKAEDA-AKAAEAAKAAEAKKAAEAKKADEAKKAAEKQQADIAKKKAEDEAKKKAEEEA 176
                                               K--AKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zamudio C,
Trawick JD,
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Malone
Carr G
                                                                                                                                                                                 36.7%; Score 190.5; DB 6; 50.4%; Pred. No. 2.7e-08; tive 14; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ਵ</u>੍ਹਿੰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haselbeck R, Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen
Forsyth
                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                 Length 372;
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                                                                                                                                                                                      13;
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Xu HH;
                                                                                                                                                                                    Gaps
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Best Local Similarity

Pred. No.

3.4e-08;

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid; (2) a host cell containing the vector; (3) an isolated cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense cell containing the vector; (3) an isolated cell polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for the gene product or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation of corganism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of compound a activity ing the target product is overexpressed or an activity of a compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for compound that proliferation of containing the extent to which each of the strains is present in a culture or collection of containing proteins or screening for homologous nucleic acids required containing an antisense nucleic acids required containing antisense nucleic acids are useful for cellular proliferation in cells other than S. aureus, S. typhimurium, contained the printed specification, but was obtained contained contained the printed specification, but was obtained contained contained the printed specification, but was obtained contained the containing the sequence data for this process.
                                ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID NO 55748; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-2001;
08-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterobacter cloacae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein encoded by Prokaryotic essential gene #13351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for homologous nucleic acids required for celisolate candidate molecules for rational drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU27824 standard; protein;
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001US-00815242.
2001US-00948993.
2001US-0342923P.
2002US-00072851.
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Carr GJ,
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  discovery
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Xu HH;
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Query Match

36.6%;

Score 190; DB

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Length 428;

Sequence 428 AA;

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the 6213 antisense sequences given in the specification where expression CC of the nucleic acid inhibits proliferation of a cell. Also included are: CC (1) a vector comprising a promoter operably linked to the nucleic acid concoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated CC polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular CC proliferation or the activity of a gene in an operon required for CC the gene product or that has an activity against a biological pathway CC required for proliferation, or that an activity against a biological pathway CC required for proliferation, or that inhibits cellular proliferation; (8) dentifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an order and that inhibits proliferation of an order and compound that inhibits are proliferation or an order and compound that inhibits proliferation of an order and compound that inhibits proliferation of an order and compound that inhibits are proliferation or an order and compound that inhibits are proliferation or an order and compound that inhibits are proliferation or an order and compound that inhibits are proliferation or an order and compound that inhibits are compound that inhibits are compound that inhibits are compound
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072891.

06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25; SEQ ID NO 56483; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang
                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ACA32429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein encoded by Prokaryotic essential gene #14086.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 AAKKAA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 KAAAEAAKKAAAAEKAAAEKAAAAEKAAADKKAAAEKAAADKKAAAEKAAADKKAAADKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 AKKAAADAQKKAEAEAAKKAAADAQKKAEAEAAKKA--AADAQKKAEAEAAKKAAQEAEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 КУАКЕААККЕАҮКАЕАККУАКААКАЕККЕУАААЕА----ККАЕААКА---УКАЕААКА 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  candidate molecules for rational drug discovery programs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELITRA PHARM INC.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Carr GJ,
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Yamamoto R,
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Forsyth RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zyskind JW;
Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
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RESULT 9
AARO6446
ID AARO
AC A
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                         To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-19 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit; 20-NOV-1984 US4691009, NRRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, protein A, and rCOP-1 sequences. A methionine residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR06446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 421 AA;
occurs between the Protein A and rCOP-1 sequences, originating
                                                                                                                                                                                                                                        Disclosure; Fig 12;
                                                                                                                                                                                                                                                                                                         Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or immunological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ06446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REPK ) REPLIGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP383620-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR06446 standard; protein; 106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1990-255848/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 AAAEAQKKAEAAAAALKKKAEAAEAAAAEARKKAATEAAEKAKAEAEKKAAAEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 АККЕАУ-КАЕАККУАКААКАЕККЕУАААЕАКК---АЕААКАУКАЕААКАААКЕАА 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKAE----KAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKXAKAEAKKYAK-EAAK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEEAAKQAELKQKQAEEAAAKAAADAKAKAEADAKA--AEEAAKKAAADAKKKAEAEAAK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   copolymer 1; COP-1-19; myelin basic protein; MBP;
al activity; autoimmune encephalomyelitis; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         copolymer 1-19, myelin basic protein analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89US-00312541.
90US-00473845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90EP-00301700
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53.0%;
                                                                                                                                                                                                                                        25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 189.5; DB 6
Pred. No. 3.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32;
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   from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protesin. rCOP-1-19 contains oligonuclectide duplexes incoding the following segments: YKK, AAE, KAK, KEA, XKA, YEA, AKA KEA, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the fusion protein. The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in certain amino acids. See also AAQ05664. (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                                                                                                      21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU47123 standard; protein; 407
                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmomella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU47123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 106 AA;
                                                                                                                            New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein encoded by Prokaryotic essential gene #32650.
                                                                                                                                                                                                                                                                               (日にココー)
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                                                                                                                                                                                        2003-029926/02
DB; ACA50993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60;
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                                                                                                                                                                                                                                                                             ELITRA PHARM INC.
                                                                                                                                                                                                                                Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKKYAKAAKAEKKEYAAAEAKKAEAA----KAYKAEAAKAAAK-EAAYE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAE 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKAAEKAKAAK-KAYEAEKAKAKYEAK--KAEKAEKAAKAAEKKAKEAKKAEK-----
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                                                                                                                                                                                                                                   Malone
Carr G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.0%;
                                                                                                                                                                                                                                  તું <sup>(</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 187; DB 2;
Pred. No. 1.4e-08;
                                                                                                                                                                                                                                  Haselbeck R, Yamamoto R,
                                                                                                                                                                                                                                  Ohlsen
Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                   Zyskind JW;
Xu HH;
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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated

The invention relates to an isolated nucleic acid comprising any one of

Claim 25; SEQ ID NO 75047; 1766pp; English.

N-PSDB; ACA35267

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RESULT 11
ABU31397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC polypeptide or its fragment whose expression is inhibited by the cartisense nucleic acid; (4) an antibody capable of specifically binding CC antisense nucleic acid; (4) an antibody capable of specifically binding CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular CC proliferation or the activity of a gene in an operon required for groliferation; (7) identifying a compound that influences the activity of CC the gene product or that has an activity against a biological pathway CC required for proliferation, or that inhibits cellular proliferation; (8) CC capable of the test compound that inhibits proliferation of an CC compound's activity; (11) a culture comprising strains in which the gene CC or a gene on which the test compound that inhibits proliferation of an CC compound's activity; (11) a culture comprising strains in which the gene CC product is overexpressed or underexpressed; (12) determining the extent CC to which each of the strains is present in a culture or collection of CC strains; or (13) identifying the target of a compound that inhibits the collection of collection of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required CC proliferation of an organism. The antisense nucleic acids are useful CC drug discovery programs, or for screening homologous nucleic acids or required for proliferation in cells other than S. aureus, S. typhimurium, CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this content did not form part of the printed specification, but was obtained CC in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                          21-MAR-2001;
06-SEP-2001;
25-OCT-2001;
WPI; 2003-029926/02
                                                                                                                                                                                                                                                           21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein encoded by Prokaryotic essential gene #16924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 407 AA;
                                                                                                                                                                                                                                                                                                     03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU31397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU31397 standard; protein; 323
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                                      'nΈ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 АККУАККАЕКАУАККАКААКЕККАУАККЕАКАУК-ААЕАКККАКАЕАККУАКЕА-АКАКК 58
                                                                                                 ELITRA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                  Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAAKAAAEAKKKAEAEAAK----AAAEAKKKADAEAAKA-AAEAKKKADAAAAKAAAEA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAYK--AEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAK---AAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKAAADAKKKAEAEAAKAAADAK--KKAEAEAVKAAADAKKKAEAEAAKAAADAKKKAEA 195
                                                                                                                                      ; 2001US-00815242.
; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                         Malone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.5%;
                                    Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 184.5; ; Pred. No. 9.4e 11; Mismatches
                                  Yamamoto R,
                                                     Haselbeck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .4e-08;
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                                  Ohlsen
Forsyth
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                                  3 2
                                  Zyskind
Xu HH;
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CC (1) a vector comprising a promoter operably linked to the nucleic acid; (2) a host cell containing the vector; (3) an isolated concleic acid; (2) a host cell containing the vector; (3) an isolated concleic acid; (2) a host cell containing the vector; (3) an isolated converge control or its fragment whose expression is inhibited by the antisence control or its fragment whose expression is inhibited by the control or its fragment whose expression is inhibited by the control or its fragment whose expression is inhibited by the control or its fragment whose expression is inhibited by the control or its gene product or that has an activity capable of specifically binding confideration; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation of corporation or the proliferation or the biological pathway in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an organism is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the gene condition of an organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational corporate for proliferation to isolate candidate molecules for rational corporation of or screening homologous nucleic acids required corporation of a compound that inhibits the cards required for proliferation in cells other than S. aureus, S. typhimurium, compound that inhibits or calls of the target prokaryotic essential genes. Note: The sequence data for this carent did not format directly from NIFO at
Matches
                                                                                                       Sequence 323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid comprising any one of
                         Local
59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25; SEQ ID NO 59321; 1766pp; English.
                         Similarity
Conservative
                   35.0%;
52.7%;
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                   Score 181.5; DB (
Pred. No. 1.3e-07
Mismatches
                                               DB 6;
34; Indels 11;
                                               Length 323;
Gaps
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103
                                                    56 -AKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
                                                                                                               47
AAKKAQQEAEKKAQQEAAKQAAAEKAAAE - KAAEKAAAQKAAAEKAAAEKAA
                                                                                                            ADAQAKAAEQAAAKAAADAK-KQAEA---AAAKAAAEAKKQAEAEAAKAAAEAQKKAEAA 102
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AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAK-----

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RESULT 12
AAY82573
ID AAY82
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AAY82573 standard; peptide; 56 Ã

AAY82573;

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.

antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic rimmune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasi glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective, osteopathic; immunosuppressive; antithyroid; antiinflammatory; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; Copolymer; molecular weight marker; TV-marker; immune disease,

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RESULT 13
AAY98499
ID AAY98
XX
AC AAY98
AC AAY98
XX
DT 31-JU
XX
DE Pepti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A AAY82571 to AAY82577 represent specifically claimed copolymer molecular CC weight TV-marker polypeptides from the present invention. The present CC invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an CC amino acid composition corresponding to the copolymer. The polypeptides CC intenting and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated CC diseases. Such diseases include arthritic conditions, demyelinating CC diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatory conditions, e.g. multiple sclerosis, crohn's CC disease, chronic immune thyroiditis, autoimmune uvecretinitis, Crohn's CC disease, chronic immune thyroiditis, autoimmune uvecretinitis, Crohn's CC sensitivity disease, dise
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                  AAY98499;
                 Peptide #10 used in nucleic acid transporter system.
                                                            31-JUL-2000
                                                                                                                                       AAY98499 standard; peptide; 100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-317499/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (YEDA ) YEDA RES & DEV CO LTD.
(TEVA-) TEVA PHARM USA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified.
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                                                                                                                                                                                                                                                                              61 УКАБАККҮАКЛАКАЕККЕУАЛАЕАККАЕЛАКАУКАЕЛАКАЛАКЕЛАУЕА 109
                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60
                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                         AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKAEAK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                            (first entry)
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 100 AA;
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WW Carcinogenesis; cardiovascular disease; infection.

XX Synthetic.

XX US6033884-A.

XX US603884-A.

XX US6033884-A.

XX US603384-A.

XX US6033884-A.

XX US6033884-A.

XX US6033884-A.

XX US6033884-A.

XX US603384-A.

XX US60384-A.

XX US60384-A
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NAY59044 standard; peptide; 100 AA.

AAY59044;

07-MAR-2000 (first entry)

Amino acid polymer seq ID NO: 64 of US5994109.

Nucleic acid transport system; NTS; cell surface receptor; cytosis; nuclear membrane; lysis moiety; transgenic animal; human disease; nucleic acid delivery; cancer.
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RESULT 15
AAB45852
ID AAB45
XX AAB45
XX AAB45
XX AAB45
XX DT 21-MA
XX Nucle
XX Nucle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a nucleic acid transport system (NTS) for CC delivering nucleic acid into a cell. The NTS contains but is not limited CC to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (C) a molety that recognizes and binds to a cell surface receptor or CC antigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a moiety that is CC capable of moving or initiating movement through a nuclear membrane; and/ CC or (e) a lysis molety that enables the transport of the entire complex CC from the cell surface directly into the cytoplasm of the cell. The NTS CC delivers nucleic acid into the cellular interior as well as the nucleus CC of specific cells. The NTS can be used to treat disorders by targeting Specific nucleic acid accordingly. The NTS can also be used to create transpent animals for assessing human disease, such as cancer, in an animal model. The NTS can be used in vitro with tissue culture cells specific expression into specifically targeted tissue culture cells. The NTS avoids the problem of endosomal/lysosomal
                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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19-MAR-1993;
14-DEC-1993;
Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme;
                                Nucleic acid transporter system peptide ligand SEQ ID NO
                                                                   21-MAR-2001
                                                                                                                               AAB45852 standard;
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Col 123-124; 107pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                     AKKYAKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAK 103
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                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                  (first entry)
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93WO-US002725.
93US-00167641.
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                                                                                                                               protein; 100 AA
                                                                                                                                                                                                                                                                                                                                                       34.6%;
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                                                                                                                                                                                                                                                                                                                                                                      Length 100;
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Search completed: April 20, Job time: 71.7792 secs

2004,

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to a cell, comprising a binding complex comprising a ligand binding CC molecule noncovalently bound to a nucleic acid and covalently linked to a CC surface ligand, and a second binding complex comprising a second binding CC muclear ligand. The complexes are simultaneously bound to the nucleic acid transporter system can also be used in a method CC for the in vivo targeting of the insertion of DNA into a cell. It can CC also be used in processes for producing transformed cell lines. The CC system can be used to deliver a variety or proteins and polypeptides, CC such as hormones, growth factors, enzymes, clotting factors, tumor antigens, viral antigens, parasitic antigens, tumor antigens, tumor CC suppressors, viral antigens, parasitic antigens, tumor antigens. The transporter system uses lysis agents to overcome the problems of CC endosomal/lysosomal degradation seen with prior art systems
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                                                                                                                                         Matches
                                                                                                                                                        Query Match
Best Local &
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19-MAR-1993;
14-DEC-1993;
                                                                                                                                                                                                            Sequence 100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid transporter system for delivering nucleic acid into a useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene; tumor antigen; tumor suppressor; viral antigen; parasitic antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Col 125-126; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-049093/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gottchalk S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bacterial antigen.
9
                                                                    μ
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AKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAK 99
                               АККУАКА-АКАЕККЕУАААЕАККАВААКАУКАЕААКААК 103
                                                                   KKAEKAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAE
                                                                                                                                         Conservative
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93WO-US002725.
93US-00167641.
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                                                                                                                                                        34.6%;
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                                                                                                                                                      Score 179.5; DB 4
Pred. No. 5.6e-08;
                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith LC,
                                                                                                                                                                       DB 4;
                                                                                                                                         34,
                                                                                                                                                                         Length 100;
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Regult
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                  228.5
190.5
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                                                                      34.5.55
34.5.55
34.5.55
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55.7
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| (ggn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
| (ggn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
| (ggn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| (ggn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| (ggn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
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         372
427
427
427
323
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347
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376
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                     US-09-816-989A-7

US-09-816-989A-6

US-09-816-989A-6

US-09-816-989A-8

12 US-10-282-122A-68109

12 US-10-282-122A-5548

12 US-10-282-122A-5648

12 US-10-282-122A-59321

US-10-282-122A-59321

US-10-282-122A-59321

US-10-282-122A-66237

14 US-10-285-132A-66237

15 US-10-285-132A-66237

16 US-10-285-132A-66237

17 US-10-285-132A-66237

18 US-10-285-979-52
                                                                                                                           Sequence 7, Appli
Sequence 6, Appli
Sequence 5, Appli
Sequence 68109, A
Sequence 55748, A
Sequence 5543, A
Sequence 75047, A
Sequence 75047, A
                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                             Sequence 5,
                                                                                    sequence 3, Appli
Sequence 66237, /
                                              Sequence
                                                                   Sequence
120, App
201, App
52, Appl
75772, A
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### ALIGNMENTS

US-09-816-989A-7 RESULT 1

Sequence 7, Application US/09816989A Patent No. US20020115103A1 GENERAL INFORMATION:

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                                                                                                                                                                                                                                       Query Match 100.0%; Score 519; DB 9; Length 109; Best Local Similarity 100.0%; Pred. No. 2.2e-34; Matches 109; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MA
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: PS-25
PRIOR APPLICATION NUMBER: D9-09-24
NUMBER: OF SEQ ID NOS: 7
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 109
61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
                                           61 YKABAKKYAKAAKABKKEYAAABAKKABAAKAYKABAAKAAAKBAAYBA 109
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US-10-282-122A-75772

Sequence

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US-09-816-989A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
                                                                                                                                                                                                                                                                                                          SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09816989A Patent No. US20020115103A1 GENERAL INFORMATION:
                                                                                        Matches
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Best Local Similarity
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Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK TITLE OF INVENTION: AND FOR THERAPEUTIC USE FILE REFERENCE: 2609/60807-A-PCT-US CURRENT APPLICATION NUMBER: US/09/816,989A CURRENT FILING DATE: 2001-03-23
                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-816-989A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/101,693
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NUMBER OF SEQ ID NOS: 7
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PRIOR APPLICATION NUMBER: PCT/US99/22402
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                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                        ENGTH:
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                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ҮКАБАККҮАҚААҚАБККЕҰАААБАҚ-КАБАА-КАҮКАБААҚАААҚБААҰБА 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , 0B
                                                                                      73; Conservative
                                           1 АККҮАККАЕКАҮАККАКААКЕККАҮАККЕАКАҮКААЕАКККАКАЕАККҮАКЕААКАККЕА 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 АККУАККАЕКАУАККАКАКЕККАУАККЕАКАУКААЕАКККАКАЕАККУАКЕААКАККЕА 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -KAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKKAYKAEAAKAAAKEAAYEA 86
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AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKA-----
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                                                                                                               55.7%;
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72.1%;

    Mismatches

                                                                                                               Score 289; DB 9;
Pred. No. 2.7e-16;
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                                                                                                                                        DB 9; Length 77;
                                                                                           3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
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TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCTUS
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                          APPLICANT: Xu, H.

TITLE OF INVENTE: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, APPLICANT: Zamu
                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 -KAEAKKYAKAAKKEYAAAEAK----YKAEAAKAAAKEAAYEA 66
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                                                                                                                                                                                                                                                                                                                                                                                                                           Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
                                                                                                                                                                                                                                                               Yamamoto, Rorsyth, R.
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Zyskind, Judith
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lio, Carlos
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56.9%; Pred. No. 1.5e-11;
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APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Cheryl
                                                                                                                                      PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/191,078
PRIOR TILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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PRIOR TILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
                                                                   PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                        PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 372
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 AKKĀĒDĀ-AKĀĀĒĀĀKĀAEĀKKĀAĒĀKKĀDĒĀKKĀĀĒKQQADIĀKKKĀEDĒĀKKKĀĒĒĒĀ 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 36.7%; Score 190.5; DB 12; Length 372; Similarity 50.4%; Pred. No. 9.1e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wall, Daniel
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Zyskind, Judith
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NUMBER: 60/267,636
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 55748
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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                                             PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
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PRIOR APPLICATION NUMBER: 60/242,578
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PRIOR FILING DATE: 2000-09-06
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 КАЛАЕЛАККАЛЛАЕКАЛЛЕКАЛЛЕКАЛЛЕКАЛЛОККАЛЛЕКАЛЛОККАЛЛЕКАЛЛОККАЛЛОКА 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INVENTION: Identification of Essential Genes in Microorganisms
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Malone, Cheryl
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Ohlsen, Kari
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Forsyth, R.
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Pred. No. 1.2e-07;
8; Mismatches 32; Indels 2:
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US-10-282-122A-75047
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     Query Match
Best Local S
Matches 66
                                                                                                                                              PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 75047
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LENGTH: 421
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PRIOR FILING DATE: 2000-03-21
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ORGANISM: Escherichia coli
                                                                                             ORGANISM: Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITLE OF INVENTION: Identification of Essential Genes in Microorganisms
ILE REFERENCE: ELITRA 034A
                                                                                                                                  ENGTH: 407
                         Local Similarity
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FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 AKKEAY-KAEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAKAAAKEAA 106
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Malone, Cheryl
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Trawick, John
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   Conservative
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 35.5%; Score 184.5; DB 12;
55.5%; Pred. No. 3e-07;
ative 11; Mismatches 25;
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25; Indels
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                                      Length 407;
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                                                                                                                                                                                                                                                                                     ) ORGANISM: Klebsiella pneumoniae US-10-282-122A-59321
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SOFTWARE: PatentIn version 3.1

SEQ ID NO 59321

LENGTH: 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 59321, Application US/10282122A Publication No. US20040029129A1
                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: U5/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23 PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
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PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/242,578
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138 AKAAADAKKKAEAEAAKAAADAK--KKAEAEAVKAAADAKKKAEAEAAKAAADAKKKAEA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 EAAKAAAEAKKKAEAEAAK----AÀAEAKKKADAEAAKA-AAEAKKKADAAAAKAAAEA 249
                                           56 - AKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
                                                                                           47 ADAQÁKAAEQÁAAKAÁADAK-KQÁEÁ---AAAKAÁAEAKKQÁEÁÉÁAKAAAEÁQKKAEAA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 EAYK--AEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAK---AAAKEAAYEA 109
                                                                                                                                                                                       59;
                                                                                                                                      1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAK-----
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                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATION NUMBER: 60/267,636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohlsen, Kari
Zyskind, Judith
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Malone, Cheryl
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                                                                                                                                                                               35.0%; Score 181.5; DB 12; 52.7%; Pred. No. 4.1e-07; tive 8; Mismatches 34;
                                                                                                                                                                                    34; Indels
                                                                                                                                                                                                                                    Length 323;
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RESULT 10

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RESULT 11
US-10-282-122A-66237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-816-989A-3
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TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
NUMBER OF SEQ ID NOS: 7
SOPTMARE: Patentin version 3.1
                                                                                                                                                                                                                                                           TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITEA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR FILING DATE: 2000-03-21
                                                                                                                       PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
                                                                         PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                PRIOR APPLICATION NUMBER: 60/242,578
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Zamudio, ca.
Zamudio, cheryl
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Forsyth, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robert
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Pred. No. 7.9e-08;
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RESULT 13 US-10-051-643-201

Sequence 201, Application US/10051643 Publication No. US20020197265A1 GENERAL INFORMATION:

APPLICANT: Watson, James D.

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US-10-127-032-120
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LENGTH: 347
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                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 170
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/127,032
CURRENT FILING DATE: 2002-04-19
CRICK APPLICATION NUMBER: US 60/285,190
PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: US 60/344,142
PRIOR FILING DATE: 2001-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Whiteley, Marvin
APPLICANT: Bangera, M. Gita
APPLICANT: Lory, Stephen
APPLICANT: Greenberg, Everet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Greenberg, Everett Peter
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF
TITLE OF INVENTION: BIOFILM FORMATION
FILE REFERENCE: UIZ-070CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                           Local Similarity
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159 A-EDEAKK--KAAEDAKKK-AAEDAKKKAAEEAKKKAAAEAAKKKAAVEA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 A-EDEAKK--KAAEDAKKK-AAEDAKKKAAEEAKKKAAAEAAKKKAAVEA 204
                                          60 АУКАБАККҮАКААКАБККЕУАААБАККАБААКАУКАБААКАААКБААУБА 109
                                                                                          99 QKLEQQQVAAAKAAEQKKADEARKAEAQKAAEAKKADEAKKAAEAKAAEQKKQADIAKKR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 АУКАЕАККУАҚААКАЕККЕУАААЕАККАЕААКАУКАЕААКАААКЕААУЕА 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 OKLEOOQVAAAKAAEQKKADEARKAEAQKAAEAKKADEAKKAAEAKAAEQKKQADIAKKR 158
                                                                                                                                       6 ККАЕКАҮАККАҚААКЕК-----КАҮАККЕАКАҮҚААЕАКККАҚАЕАККҮАКЕААКҚЕ 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 49.1%;
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b. US20030113742A1
                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                         34.5%; Score 179; DB 14; 49.1%; Pred. No. 6.9e-07;
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                                                                                                                                                                                     17; Mismatches
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                                                                                                                                                                                     Indels 10;
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                                                                                                                                                                                Gaps
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US-10-282-122A-75772

Sequence 75772, Application US/10282122A

Publication No. US20040029129A1

; GENERAL INFORMATION:
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                                                                                                       RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT ; ORGANISM: Mycobacterium vaccae US-10-205-979-52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 52
LENGTH: 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 52, Application No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
APPLICANT: Tan, Paul L. J.
APPLICANT: Tan, Paul L. J.
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANTON: Compounds and Methods for the Modulation TITLE OF INVENTION: of Immune Responses
FILE REPERENCE: 11000.1063U
CURRENT APPLICATION NUMBER: US/10/205,979
CURRENT APPLICATION NUMBER: 007-25
PRIOR APPLICATION NUMBER: 60/308,446
PRIOR APPLICATION NUMBER: 60/308,446
PRIOR FILING DATE: 2001-07-26
NUMBER OF SEQ ID NOS: 52
NUMBER OF SEQ ID NOS: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 201
LENGTH: 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 11000.1008c2
CURRENT APPLICATION NUMBER: US/10/051,643
CURRENT FILLING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US09/156,181
PRIOR FILLING DATE: 1198-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 08/996,624
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tan, Paul L. J.

ITTLE OF INVENTION: Methods and Compounds for the Treatment

ITTLE OF INVENTION: of Immunologically Mediated Diseases of the Respiratory

ITTLE OF INVENTION: System using Mycobacterium Vaccae
                                                                                                                                                                                 171
                                                                                                                                                                                                                                                                        112 АККЛАККАРАККАЛАККАЛРАККАРАККА-АТКЛАРАККАТЛАККАЛАРАККАТЛАККАЛР 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 ARKAAKKAPAKKAAAKKAAPAKKAPAKKA-ATKAAPAKKATAAKKAAPAKKATAAKKAAP 170
                                                                                                                                                                                                                   56 AKKEAYKAEAKKYAKAAKAEKKEYA--AAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                                                                                                                                                                                                                                                          ch 34.3%;
1 Similarity 54.5%;
60; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 АККЕЛҮКАЕЛККҮЛКАЛКАЕККЕҮЛ--ЛЛЕЛККАЕЛЛКАУКЛЕЛЛКАЛАК 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKK--AEKAYAKKAKAAKE---KKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity
60; Conserv
                                                                                                                                                                                                                                                                                                                        AKKYAKK--AEKAYAKKAKAAKE---KKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAK 55
                                                                                                                                                                           Application US/10205979
No. US20030147861A1
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                                                                                                                                                                                                                                                                                                                                                                     Score 178; DB 14; Length 223; Pred. No. 5.2e-07; 6; Mismatches 34; Indels 1
                                                                                                                                                                                                                                                                                                                                                                          Indels 10;
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Search completed: April 20, 2004, 23:27:18 Job time : 54.7922 secs
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/215,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PRILING DATE: 2000-12-29
PRIOR PRILING DATE: 2000-12-29
PRIOR PRILING DATE: 2000-12-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-282-122A-75772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Remaining Prior Application data removed - See File Wrapper or PALM
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 75772
                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITLE OF INVENTION: Identification of Essential Genes in Microorganisms ILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                   191
                                                                                                                                                                                                                                         137 AKAAADAKKKAEAEAAKAAADAKKKAEAEA-AKAAADAKKKAEAEA---AKAAAEAKK--
                                                                                                                                                                         61 УКАЕАККУАКЪАКАЕККЕУЉЪЉЕАККАЕЉАКАУКЪЕЉАКЉЪ --- КЕЉАУЕ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376
                                                                                                                                                                                                                                                                                                1 АККҮАККАЕКАҮАККАКААКЕККАҮАККЕАКАҮКААЕАКККАКАЕАККҮАКЕААКАККЕА 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carr, Grant
Carr, Grant
Carr, Grant
                                                                                                                   -KAEAEAAKAAADAKKKADAEAAKAAAEAKKKADAAAAKAAADAKKKAAAE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wall, Danie.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                         34.3%; Score 178; DB 12; Length 376; 52.3%; Pred. No. 9e-07; ative 10; Mismatches 33; Indels 1
                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                            Gaps
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FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
INUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5390
LENGTH: 361
TYPE: PRT
ORGANISM: Proteus mirabilis
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                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-216-894-8
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US-08-216-894-8
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                                                                                               Query Match 31.3%; Score 162.5; DB 2; Length 643; Best Local Similarity 44.4%; Pred. No. 2e-06; Matches 52; Conservative 18; Mismatches 36; Indels 11
                                                                                                                                                                                                                                                 TELEFAX: (202)672-5399
TELEZ: 904136
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 643 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08216894 Patent No. 5876734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.6%; Score 169; DB 4; Length 361; Best Local Similarity 44.0%; Pred. No. 3.2e-07; Matches 51; Conservative 16; Mismatches 37; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
445 AABATKVABABKQKAABATKVABABKQKAABATKVABABKQKAABATKVABABKQKAABA 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 AKEAAEAQRREAATAAAKAKEEQKQAEEAAAQAKAERDRILKEQADAKAKAEAEAKKQAE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 LAAKOKAEEAKAKAEAEAKAKAEADAKAKAEADAKAKAAAEAKAKAAAEAKAAAOO 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 ЕААКАККЕАҮКАЕАККҮАКА---АКАЕККЕҮАААЕАККАЕААКАҮКАЕААКААКА 104
                                               1 АККҮАККАЕКАҮАККАКАККАКАКККАҮАККЕАКАҮКА-----АБАКККАКАБАККҮАК 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                  Indels 11; Gaps
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Search completed: April 20, 2004, 23:19:08 Job time: 23.6494 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-252-991A-29581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATI
TITLE OF INVENTION: AERIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US/60/074,788
PRIOR PILING DATE: 1998-07-18
PRIOR APPLICATION NUMBER: US/09/094,190
PRIOR APPLICATION NUMBER: US/09/094,190
PRIOR APPLICATION DATE: 1998-07-27
NUMBER: OF SEQ. ID NOS: 33142
               APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Compounds and Methods for TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections NUMBER OF SEQUENCES: 208

CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Skinner, Margot APPLICANT: Prestidge, Ross
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/095,855 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 49.1%;
                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 A-EDEAKK--KAAEDAKKK-AAEDAKKKAAEEAKKKAAAEAAKKKAAVEA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 OKLEOOQVAAAKAAEOKKADEARKAEAOKAAEAKKADEAKKAAEAKAAEOKKOADIAKKR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 AYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 КҚАБҚАҰАҚҚАҚААКБК-----ҚАҰАҚҚБАҚАҰҚААБАҚҚҚАҚАБАҚҚҰАҚБДАҚАҚКБ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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206-269-0565
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N: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.5%; Score 179; DB 4;
49.1%; Pred. No. 5.2e-08;
                                                                                                                                                                                                                                                                        08/705,347
                                               11000.1002c3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 407;
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US-09-543-681A-5390
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 201
LENGTH: 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 201, Application US/09205426 Patent No. 6406704
                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                           Best
                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER FILING DATE: 1998-06-11
EARLIER APPLICATION NUMBER: 08/997,362
EARLIER FILING DATE: 1997-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/205,426
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 09/095,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Compounds and Methods for Treatment and TITLE OF INVENTION: Diagnosis of Mycobacterial Infections FILE REFERENCE: 11000.1002c4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER FILING DATE: 1996-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1997-06-12 EARLIER APPLICATION NUMBER: 08/705,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Watson, James D. APPLICANT: Tan, Paul L. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: 08/873,970
                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Mycobacterium vaccae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 206-269-0563
TELEX:
                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 34.3%;
Local Similarity 54.5%;
                                                                                  112 ARKAAKKAPAKKAAAKKAAPAKKAPAKKA-ATKAAPAKKATAAKKAAPAKKATAAKKAAP 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 ARKAAKKAPAKKAAAKKAAPAKKAPAKKA-ATKAAPAKKATAAKKAAPAKKATAAKKAAP 170
                                                                                                                          56 AKKEAYKAEAKKYAKAAKAEKKEYA--AAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 AKKEAYKAEAKKYAKAAKAEKKEYA--AAEAKKAEAAKAYKAEAAKAAAK 103
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                                                                                                                                                                                                           1 AKKYAKK--AEKAYAKKAKAAKE---KKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAK 55
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                                                                                                                                                                                                                                                                34.3%;
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Pred. No. 3.5e-08;
6; Mismatches 34
                                                                                                                                                                                                                                                     6; Mismatches
                                                                                                                                                                                                                                                                       Score 178; DB 4; Length 223; Pred. No. 3.5e-08;
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GENERAL INFORMATION:
APPLICANT: GARY BRETON
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

Sequence 5390, Application US/09543681A Patent No. 6605709

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                                                                                                                                                              Query Match
Best Local Similarity 55.0%;
                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,971A
FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Suic
STREET: Los Angeles
CITY: Los Angeles
CTATE: California
" S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: WOO, SAVIO L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                          OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                 65 АККҮАКА-АКАЕККЕҮААЛЕАККАЕЛАКАҮКАЕЛАКАЛАК 103
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ККАЕКАУАК-КАКААКЕККАУАККЕАКАУКААЕАКККАКАЕАККУАКЕААКАККЕАУКАЕ 64
                                                                                                                                                                                                                                                                                                                                                                        100 amino acids
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633 West Fifth Street
                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              (213) 955-0440
                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                         "Lys Ala" in positions 3 to 100 may be present or absent.
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                                                                                                                                              Score 179.5; DB 3
Pred. No. 1.2e-08;
8; Mismatches 34
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                                                                                                                                                                                  DB 3; Length 100;
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                                                                                                                                              Indels
                                                                                                                                            3; Gaps
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US-08-462-040-64
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                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/462,040
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION UMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Marburg, Richard J.
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 312/078
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                  OTHER INFORMATION: "Lys Ala" in positions 3 to OTHER INFORMATION: present or absent.
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
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5. 6177554
60 AKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAK 99
                                        65 AKKYAKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                           6 ККАЕКАУАК-КАКААКЕККАУАККЕАКАУКААЕАКККАКАЕАККУАКЕААКАККЕАУКАЕ 64
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cristiano, Richard J.
Gottchalk, Stephen
VENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Compatible
                                                                                                                                                                        34.6%; Score 179.5; DB 3; 55.0%; Pred. No. 1.2e-08; ative 8; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM P.C. DOS 5.0
                                                                                                                                                                                                                     Length 100;
                                                                                                                                                                                                                                                                                                             100 may
                                                                                                                                                                        Gaps
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RESULT 11 US-09-252-991A-29581 ; Sequence 29581, Application US/09252991A

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; OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be ; OTHER INFORMATION: present or absent. US-08-460-890A-64
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                                                  Query Match
Best Local Similarity
                                          Matches
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                                                                                                                                                                                                                                                               TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DALE.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/167,641
PRIOR TOATION NUMBER: 14, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           CELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                          TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
                                                                                                                                                                                                                 STRANDEDNESS:
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STREET: Solite 4700
CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                   COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                            NAME: Warburg, Richard
REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                         55; Conservative
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6 KKAEKAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAE 64
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Gottchalk, Stephen
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Smith, Louis C.
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                                   34.6%; Score 179.5; DB 2; 55.0%; Pred. No. 1.2e-08; tive 8; Mismatches 34;
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                                                                                                                    Matches
                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                     MOLECULE TYPE:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: March 20,
APPLICATION NUMBER: PC
FILING DATE: March 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITLE OF INVENTION: NUCLEIC ACID TO
                                                                                                                                                                                                 OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may OTHER INFORMATION: present or absent.
                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0
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OPERATING SYSTEM:
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STATE: California
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STREET: 633 West Fifth Street
STREET: Suite 4700
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65 AKKYAKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAK 103
                                                   65 АККУАКА-АКАВККЕУАЛАВАККАВЛАКАУКАВЛАКАЛАК 103
                                                                                 6 ККАЕКАУАК-КАКААКЕККАУАККЕАКАУКААЕАКККАКАЕАККУАКЕААКАККЕАУКАЕ 64
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Smith, Louis C.
Cristiano, Richard J.
Gottchalk, Stephen
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                                                                                                                                  34.6%; Score 179.5; 55.0%; Pred. No. 1.2
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                                                                                                                  Mismatches
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US-09-405-743A-4
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LENGTH: 77
TYPE: PRT
                                                                                                              SOFTWARE: P.
SEQ ID NO 4
LENGTH: 66
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APPLICANT: Yeda Reservitue:
TITLE OF INVENTION:
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Best Local Similarity
Matches 80; Conserv
                                                                                                                                                                  APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION UNMESE: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
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CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
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                OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE
                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                        PatentIn Ver. 2,1
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VENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.7%; Score 289; DB 4; 67.0%; Pred. No. 6.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
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Pred. No. 7.8e-20;
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    3; Indels 27;

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CURRENT FILING DATE: 209/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13555
LENGTH: 469
                                                                                                                         SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 56
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
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Patent No. 6610836
Query Match
Best Local Similarity
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CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
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Best Local &
                                                                                                                                                                                                                                                                                                                           FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAB FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                       OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 51.2 hes 62; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 AKAKKEAYKAEAKKYAKA---AKAEKKEYAAAEAKKAEAAKAYKA--EAAKAAAKEAAYE 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
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                                                                                     Description of Artificial Sequence: PEPTIDE
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34.8%;
45.9%;
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Score 180.5; DB 4
Pred. No. 5.4e-09;
                    DB 4;
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Scoring table: Sequence:

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Perfect score:

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Sequence 4, Appli Sequence 3, Appli Sequence 5, Appli Sequence 22853, Appli Sequence 3, Appli Sequence 5734, Appli Sequence 5734, Appli Sequence 27, Appli Sequence 27, Appli Sequence 62, Appl Sequence 62, Appli Sequence 62, Appli

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Minimum DB seq length: 0
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Copyright (c) 1993 - 2004 Compugen Ltd
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US-08-4160-890A-64
US-08-4160-971A-64
US-08-4160-971A-64
US-08-420-400-64
US-09-252-991A-29581
US-09-255-426-201
US-09-254-426-201
US-09-254-426-201
US-09-254-426-426
US-09-417-264-42
US-09-417-264-32
US-09-115-746-10
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5390, Ap
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8, Appli
40, Appl
              Sequence 6, Application US/09405743A

Patent No. 6514938

GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
ITILE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILLING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 86
TYPE: PRT
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CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 109
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
ORGANISM: Artificial Sequence
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US-09-911-889-3
US-08-837-058-3
US-09-417-264-3
US-09-417-264-3
US-09-489-039A-13743
US-09-041-889-27
US-09-0417-264-27
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Pred. No. 5.6e-37;
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Match

Query

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289 228.5 519 312.5 Score